

STIC-Biotech/ChemLib

71738

From: Collins, Cynthia
Sent: Wednesday, 4/24/2002 4:59 PM
To: STIC-Biotech/ChemLib
Subject: sequence search request SN 09/828447

Please search, both prior art and interference, for SN 09/828447:

1) SEQ ID NO:12
2) SEQ ID NO:7

Thank You,

Cynthia Collins
Art Unit 1638
CMI, 9A12 (office) or 9E12 (mailbox)
(703) 605-1210

Edward Han
Technical Info. Specialist
STIC/Biotech
CMI 6B02 Tel: 305-9203

4/6/01
prev 4/7/00
1026 4/7/99

TYPE OF SEARCH:

NA Sequences: ☒
AA Sequences: ☒
Structures: ☒
Bibliographic: ☒
Litigation: ☒
Full text: ☒
Patent Family: ☒
Other: ☒

VENDOR/COST (where applic.)
STN:
DIALOG:
Questel/Orbit: ☒
DRLink: ☒
Lexis/Nexis: ☒
Sequence Sys.: ☒
WWW/Internet: ☒
Other (specify): ☒

Searcher:

Phone:

Location:

Date Picked Up:

Date Completed: 4/24/02

Searcher Prep/Review: 4/24/02

Clerical:

Online time:

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 26, 2002, 13:07:56 ; Search time 2533.87 Seconds

(without alignments)

11393.634 Million cell updates/sec

Title: US-09-828-447-7

Perfect score: 2139

Sequence: 1 atccgggcttcgggagttt.....gtgcacccaaggttaacgcc 2139

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: em_estba:*
2: em_esthm:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrc:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	298.8	14.0	419	10	BJ194081
2	284.8	13.3	496	9	AW561280
3	281.2	13.1	706	10	BJ167090
4	251.2	11.7	540	10	BJ163593
5	183	8.6	551	10	BJ206977
6	181.6	8.5	543	10	BJ160350
7	176.2	8.2	659	10	BJ1265786
8	173.2	8.1	783	10	BG646260
9	171.6	8.0	775	10	BG595783
10	167.2	7.8	617	9	AW277493
11	163.4	7.6	772	10	BE822903
12	156.8	7.3	606	9	A1938235
13	156.2	7.3	838	9	AW448540
14	155	7.2	527	10	BG381790
15	154.2	7.2	655	10	BF637852
16	152.4	7.1	421	9	AW496918
17	149.4	7.0	716	10	EG644550

18	147.6	6.9	871	9	BE040051
19	145	6.8	716	10	BG645186
20	141	6.6	757	10	BI177154
21	138	6.5	586	9	AW561394
22	136	6.4	805	10	BI920569
23	135.8	6.3	761	10	BI969233
24	134.8	6.3	589	9	AV536140
25	133.6	6.2	628	9	AW774900
26	130.4	6.1	589	9	BE036525
27	130.4	6.1	764	9	A1794656
28	128.8	6.0	582	9	AW564895
29	126.6	5.9	607	9	AW164281
30	126	5.9	635	9	AU108535
31	125.8	5.9	455	10	BJ175092
32	123.8	5.8	646	10	BG595391
33	119.8	5.6	493	10	BF069301
34	119.6	5.6	496	10	BJ192301
35	119	5.6	477	10	BJ193355
36	116.6	5.5	397	10	BG137605
37	115.6	5.5	823	10	BF267475
38	114	5.3	649	9	AW685378
39	113.8	5.3	557	9	AW257926
40	111.8	5.2	597	9	A1485566
41	107.8	5.0	436	9	A1948076
42	107.6	5.0	554	9	AW735896
43	107.4	5.0	615	10	BG136556
44	106	5.0	681	9	AW774123
45	105.2	4.9	555	10	BI699487

ALIGNMENTS

RESULT 1

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BJ194081 419 bp mRNA linear EST 24-JAN-2002
BJ194081 normalized full length cDNA library, chloronemata, caulonemata and rhizoid-like protonemata Physcomitrella patens subsp. patens cDNA clone pphnlh22 5', mRNA sequence.
BJ194081
BJ194081.1 GI:18362014
EST.
Physcomitrella patens subsp. patens.
Physcomitrella patens subsp. patens
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta; Bryopsida; Funariaceae; Funariales; Funariaceae; Physcomitrella.
1 (bases 1 to 419)
Fujita, T., Shin-i, T., Seki, M., Kamiya, A., Uchiyama, I., Nishiyama, T., Carninci, P., Hayashizaki, Y., Shinozaki, K., Kohara, Y. and Hasebe, M.
Comparison of the moss Physcomitrella patens genome with flowering plants genome
Unpublished (2002)
Contact: Tadasi Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp
A backbone of the vector is pBluescript II, that was in vivo excised from a modified LPS phage vector (Mo bi Tec, Germany). XhoI digested-5' end of cDNA is ligated to SalI site of the vector, and the BamHI digested-3' end including poly-A tail is ligated to BamHI site of the vector. cDNA insert could be amplified with conventional T7 and T3 primers. This normalized full-length cDNA library was generated basically according to the method described in Genome Research 10, 1617-1630 (2000), Carninci, P. et al. Protonemata were blended by the POLYTRON, and then cultivated on the BCD medium containing 1mM NAA (naphthalene acetic acid) for 8 to 11 days under the continuous light.

FEATURES

Location/Qualifiers

1. .419

source

/organism="Physcomitrella patens subsp. patens"
 /db_xref="taxon:145481"
 /clone="pbnh22"
 /clone_lib="normalized full length cDNA library,
 chloronemata, caulonemata and rhizoid-like protonemata"
 /tissue_type="mixture of chloronemata, caulonemata and
 rhizoid-like protonemata"
 BASE COUNT 96 a 75 c 145 g 103 t
 ORIGIN

Query Match 14.0%; Score 298.8; DB 10; Length 419;
 Best Local Similarity 99.0%; Pred. No. 1.3e-74;
 Matches 311; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
 QY 7 ggtctggaggttaagagatgtcacggcgtgggaagacgagcggtgatcaggtttg 66
 Db 106 GACTTCGGGAGTTTAAAGAGGATGTCAGCGGTGGGAAGACGAGCGGTGATCGAGTTG 165
 QY 67 ggtgagacttaaggtgacgaggtgtaaggatgcgctcgtcactgggtttgcaaaatgt 126
 Db 166 GTTGAGGCTTAAAGTTGACGGAGTGAAGGGATCGGCTGCTCAGTGGTTTCAAAATGT 225
 QY 127 gtctcatagcatgtgtcgaagtgggaaccccaagggatccggagcaagacctggt-g 185
 Db 226 GTTCCATAGCATGTTGTCGAGTGGAAACCCCGAAAGGGGATCCGGAGCAAGACCTGGTGG 285
 QY 186 ggggaggtgtcacatatatagcagcgaagatgagagatgagtcgaggggtgtgtgaaa 245
 Db 286 GGGGAGGTGTTCACATATATACAGCAGAGATGAGAGATGAGTGGCGGAGGGTGTGTGAAA 345
 QY 246 ttcttcacacagacgaagggtgtcgaactcactcactccttgatgcgccaagcagatcatg 305
 Db 346 TTCTTCATACAGCAAGGGATGTCGACTTCACCTTGTATGACGCCAAGCAGATCATG 405
 QY 306 gagcgattcga 319
 Db 406 GAGCGCATTCGCAA 419

RESULT 2

AW561280 496 bp mRNA linear EST 08-MAR-2000
 LOCUS ga78a1.y1 Moss EST library PPU Physcomitrella patens cDNA clone
 DEFINITION PEP SOURCE ID: PPU140521.5, similar to TR:Q43442 Q43442
 PHOSPHONOSIIDE-SPECIFIC PHOSPHOLIPASE C P12. /; mRNA sequence.

ACCESSION AW561280
 VERSION 1
 KEYWORDS EST.
 SOURCE AW561280.1 GI:7207277
 ORGANISM Physcomitrella patens.

REFERENCE AUTHORS
 Quatrano, R., Bashardes, S., Cove, D., Cuming, A., Knight, C., Clifton
 S., Marra, M., Hillier, L., Pape, D., Martin, J., Wylie, T., Underwood
 K., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T.,
 Steptoe, M., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R.,
 Waterston, R. and Wilson, R.
 Leeds/Wash U Moss EST Project
 Unpublished (1999)

TITLE
 JOURNAL
 COMMENT
 Contact: Ralph Quatrano
 Leeds/Wash U Moss EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu

Libraries were constructed by Dr. Stavros Bashardes as part of the
 Physcomitrella EST program (PEP) at the Univ. of Leeds (UK) and
 Washington Univ. in St. Louis (USA) DNA sequencing by: Washington
 University Genome Sequencing Center For information on obtaining a
 clone please contact: Celia Knight (c.d.knight@leeds.ac.uk)

Seq primer: -40RP from Gibco
 High quality sequence stop: 309.
 Location/Qualifiers
 1. 496
 /organism="Physcomitrella patens"
 /db_xref="taxon:3218"
 /clone="PEP_SOURCE_ID:PPU140521"
 /clone_lib="Moss EST library PPU"
 /tissue_type="protonemata: 7 day old tissue
 ammonium-grown"
 /lab_host="DH10B"
 /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
 XhoI; Construction of the cDNA library was carried out
 using Strategenes 'UnizAP - cDNA synthesis kit'. cDNA
 was constructed using an oligo dt primer/linker that
 contains a XhoI site within it. Following ds cDNA
 synthesis, EcoRI adapters were ligated to the blunt ends
 and sample was digested with XhoI. The result is cDNA
 with an EcoRI sticky end on one side and a XhoI sticky
 end on the other. This cDNA was ligated directionally in
 UnizAP arms. The vector is designed containing the
 pBluescript sequence as well as lambda DNA and cDNA is
 cloned within this pBluescript sequence. The vector was
 then packaged using Gold gigapackaging extracts. Library
 was grown in XL1Blue MRP cells and amplified. The library
 was excised by mass excision using Strategenes 'Mass
 excision kit' that uses exassit as a helper phage that
 releases the pBluescript sequence and circularizes it as
 single stranded plasmids that are then packaged (by helper
 phage) and secreted out of the host cell as phagemids.
 SOLR cells were transformed with phagemids and the library
 was plated out on LB-amp plates to select for
 transformants. Approximately 1,000,000 colonies were grown
 and recovered. The double stranded plasmid library was
 recovered by using Quiagen Midi prep kit. 2 micro grams of
 each library were used to transform DH10B cells by
 electroporation."

BASE COUNT 148 a 105 c 126 g 117 t
 ORIGIN

Query Match 13.3%; Score 284.8; DB 9; Length 496;
 Best Local Similarity 73.4%; Pred. No. 1.5e-70;
 Matches 364; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

QY 1454 gctttggcaggcatttgcaagttcaagggaatggggatgtgggtatgttttgaagcc 1513
 Db 1 GCTCTGGCAAGCCACGCCAAGTTCAGGGGAATGGTGTGTGATACATCCTTAAGCC 60

QY 1514 acagtatctgttgaaacttgccttctgtgtgcttttcaaccaccatcacccagaaa 1573
 Db 61 AAAGTATCTATTGGAAGATTGGCCCAATGGTAACCTTTTAACCCCTTACGCTCCTGGAGA 120

QY 1574 cacaaccttaattcgaagataaagtattgaactccttgggagggacaaagccttttc 1633
 Db 121 TACAAGATGATCTTGAAGGTAAAGGTAATACAGCATGGGATGGACAAAAGCGTTCC 180

QY 1634 caaacgccatttgacattctcaccctcagatttctcactaggttgattgtgtgtgg 1693
 Db 181 CAATACCATTTCAACCTTTACTCGCCTCCAGATTTCCTTCACTAGGCTGCTTGTGACTGG 240

QY 1694 agtgcctgctgacgagggcccaagtgggaagacatctgtggtggacaattcatggcaccaca 1753
 Db 241 AGTGCCTGCCGATGTGGCAAGTGGAAATCTCCGTTATAGATGACATTTGGGAACCCCA 300

QY 1754 ttggaatgagaccatgagtttgccttaaatgcccctagctcgcactacttcgcacoga 1813
 Db 301 CTGGAACGAGGATCACAGGATTATACCTGAAATGCCCTTGAACCTTGCATGCTCCGAATGA 360

QY 1814 ggtccgagaccatgatgatgacaaagatgatttgaagggcagacatgccttcccat 1873
 Db 361 AGTTAGAGATCAGCAGGAGAAAGTCAAGTAGTTCGAAGGGCATGCGTCCCTTCCAAT 420

	Db	586	TGGGACAAAGCGTTCCCAATACCATTTCGCCCTTTCGCCTCACAATTTCTTCACT	527
	QY	1677	aagtgatggtggaggctgcctgcgaacccaaagtgaacacctgtgtgatc	1736
	Db	526	AGGTGCTTGACTGAGTGCTGCGCATGTGGAAGTGGAAAACCTTCGTTATAGAT	467
	QY	1737	aattcatcgcccccaattgaatgagaccatgatttttgccttaaaaatgccctgagtc	1796
	Db	466	GACGTTTTGGGAACCCCACCTGGAACGAGNACACAGATTTTACCTTAATAATGCCCTGAACCT	407
	QY	1797	gcactacttcgcacgagctccgcagaccatgatgatataagaagatgattttaaggg	1856
	Db	406	GCACCTCTCGAATTCAGTTAGATCACGACGAGGAAGAATCAAGTAGTTCGAAGGG	347
	QY	1857	cagacatgcctcccacccaatgcgagatggttatcggtgcataatgataaac	1916
	Db	346	CAGGCGTGCCTCCAATGCTGAATTAAGACGGCTATCGATGCGTCAGATGTATGAC	287
	QY	1917	aagtagggcaatgtactgaaaggcgtgctgatatgttgttttcatttcaaaa	1966
	Db	286	AAAAAGGCGACGTGTGTGAAGGCGTGAAAAATGTTGTTCCATTTTCAA	237
	RESULT	4		
	BUI67090/c			
	LOCUS	BUI67090 full length cDNA library, chloronemata and young gametophores Physcomitrella patens subsp. patens cdna clone pphl4al5 3', mRNA sequence.	540 bp	mRNA linear EST 24-JAN-2002
	DEFINITION			
	ACCESSION	BUI67090		
	VERSION	BUI67090.1 GI:18335072		
	KEYWORDS	Physcomitrella patens subsp. patens.		
	SOURCE	Physcomitrella patens subsp. patens Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta; Bryopsida; Funariaceae; Funariales; Funariales; Funariaceae; Physcomitrella. 1 (bases 1 to 706) Fujita,T., Shin-I., Seki,M., Kamiya,A., Uchiyama,I., Nishiyama,T., Carninci,P., Hayashizaki,Y., Shinozaki,K., Kohara,Y. and Hasebe		
	REFERENCE	Comparison of the moss Physcomitrella patens genome with flowering plants genome. Unpublished (2002)		
	AUTHORS	Contact: Tadasu Shin-i Center For Genetic Resource Information National Institute of Genetics 111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855		
	JOURNAL	Email: tschini@genetics.nig.ac.jp		
	COMMENT	A backbone of the vector is basically from pBluescript(KS), that was in vivo excised from a modified lps phage vector (Mo bi Tec, Germany). 5' end of the cDNA that was digested with XhoI was ligated to SalI site of the vector and the 3' end including polyA tail was ligated to BamHI site of the vector. cDNA insert could be amplified with conventional T7 and T3 primers. This full-length cDNA library was generated basically according to the method described in The Plant J 15, 707-720 (1998) Seki M. et al. Protonemata were blended by the POLYTUN, and then cultivated on the BCDAT medium for 13-14 days under the continuous light.		
	FEATURES	Location/Qualifiers		
	source	1..706		
		/organism="Physcomitrella patens subsp. patens"		
		/db_xref="taxon:145481"		
		/clone_lib="full length cDNA library, chloronemata and young gametophores"		
		/tissue_type="mixture of chloronemata and young gametophores with 2 to 5 leaves"		
	BASE COUNT	188 a 175 c 142 g 200 t		
	ORIGIN			
		Query Match 13.1%; Score 281.2; DB 10; Length 706;		
		Best Local Similarity 74.9%; Pred. No. 2.1e+69;		
		Matches 352; Conservative 0; Mismatches 118; Indels 0; Gaps 0;		
	QY	1497	gggtatgttttgaaggcacagatctgttggaacttcctctgtgtgtgccttcaac	1556
	Db	706	GGATACATCTTAAGCCAAAGTATCTATTGGAAGATTTCCCAATGGTAAACCTTTAAAC	647
	QY	1557	ccacatcacccacaagaacacocctaattctcaagattaagattaatgactacttgga	1616
	Db	646	CCTTCAGTCTTGAGATACCAAGATCTTTCAGGTAAAGTAAATGACAAACCGGGA	587
	QY	1617	tgggacaaggccttttccaaacgcacatcttcgaactatctccacccagatttctact	1676

Query Match 11.7%; Score 251.2; DB 10; Length 540;
Best Local Similarity 70.0%; Pred. No. 7.7e-01;
Matches 353; Conservative 0; Mismatches 148; Indels 3; Gaps 1;

QY 80 gttgacgcagtgtaaggatcggtctcactgggttgcataatgtgttcattgatcatg 139
Db 37 GGTGTCGAGGGATTTATTGTCCGTAGCTGGGTTGCATAAANGTGTCTATTCCGTT 96

QY 140 ttgtcgaagtgtgaaccgccaaagggatccgagcaaaccttgggtggggagggtttcac 199
Db 97 CGGTCCGAAGAAGTCCAAGAAGGGGATTTGCCGACAGATCATTTGGGGGATGTGTCTC 156

QY 200 aatatacagcgagaatgagagagtagtcgaggggttgcataatcttgcatacaga 259
Db 157 GACTTACAGCGAGAATGGGAAGCTTGACGCCGAGGGGTGCTGAAGTCTTTGCAGACAGA 216

QY 260 gcaagggaatgtcgactccaccttgatgacgccaagcagatcatgagcgactcgcaa 319
Db 217 GCAGGGGATAGCAAGTCTCTTAGATGACGCCAACCATTTAGTGGAGTGTGATTCGGAA 276

QY 320 ggactggaagaaatccttcggactcgactctctaaaactcagacttgtcgaagcgagc 376
Db 277 TGAGAGACATAAGTCGAAATTCCTGGGTTTCATCGTCAGTCGAGACTCTCGAAGGGTGA 336

QY 377 ttttcggaagtactgatgaatcccgacttgatgacgccaagcagatcatgagcgactcgcaa 319
Db 337 TTTTAAAACATATGTACTGAGCCCGGATTTCAATGGGGTCTTTGTAAGCACTGTGCATCA 396

QY 437 agaatgacgcagcggatgtcgactactttcattacacgcccataactcgactcgactgcac 496
Db 397 AGACATGACGACGGCGTTATGCGCACTACTTCATATTCTAGTGTCAACAACCTGACTTGAC 456

QY 497 cggcaacagctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 556
Db 457 GGTTAAACAGCTTAGCAGCCACAGTAGCAGCGCTCCCATTGCTGCTGCACTGCAACGTGG 516

QY 557 cgtcgaggtgtggaattggaactt 580
Db 517 CGTCGGGTGTGGAACCTGGATTT 540

RESULT 5

BJ206977 551 bp mRNA linear EST 25-JAN-2002

LOCUS BJT206977 normalized full length cdna library, chloronemata,
DEFINITION caulonemata and rhizoid-like protonemata Physcomitrella patens
subsp. patens cDNA clone pphn3915 5' mRNA sequence.

ACCESSION BJT206977

VERSION BJT206977.1 GI:18375399

KEYWORDS EST.

SOURCE Physcomitrella patens subsp. patens.
ORGANISM Physcomitrella patens subsp. patens.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Kryptosida; Funariidae; Funariales; Funariaceae; Physcomitrella.
Fujita,T., Shin-I.T., Seki,M., Kamiya,A., Uchiyama,I., Nishiyama,T.
M., Carninci,P., Hayashizaki,Y., Shimozaki,K., Kohara,Y. and Hasebe
Comparison of the moss Physcomitrella patens genome with flowering
plants genome
Unpublished (2002)
Contact: Tadasi Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tschini@genes.nig.ac.jp
A backbone of the vector is pBluescript II, that was in vivo
excised from a modified lps phage vector (Mo bi rec, Germany). XhoI
digested-5' end of cDNA is ligated to SalI site of the vector, and
the BamHI digested-3' end including poly(A tail) is ligated to BamHI
site of the vector. cDNA instert could be amplified with

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseolaceae; Glycine.

1. (bases 1 to 772)
Wodkin, L., Keim, P., Shoemaker, R., Retzel, E., Khanna, A., Coryell, V.,
Erdelding, J., Raph, C., Shoop, E., Pardinas, J., Liu, L. and Lewin, H.
A Functional Genomics Program for Soybean (NSF 9872565)
Unpublished (1999)

Other ESTs: AW164281 corresponding to Gm-cl023-42 (5')
Contact: Vodkin, L.O., PI, A Functional Genomics Program for Soybean (NSF 9872565)
Lewin, H. A., Director, Keck Center for Comparative and Functional Genomics

Department of Computer Science
University of Illinois
Adwin R. Madigan Building, 1201 W. Gregory, Urbana, IL 61801, USA
Tel: (217) 244-6147
Fax: (217) 333-4582

email: l-vodkin@uiuc.edu
This clone is available through: Genome Systems, Inc. 4633 World
Highway Circle St. Louis, Missouri 63134. For further information
call: (800) 430-0030 or (314) 427-3222 FAX: (888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or [info@genome
systems.com](mailto:info@genome
systems.com) Web site: www.genomesystems.com
© 1998, Genome Systems, Inc.

eq primer: 5'-TTTTTTTTTTTTTTTTT(A/C/G)-3'.

Location/Qualifiers
1. .772

```

/organism="Glycine max"

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/db_xref="taxon:3847"

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/clone="Gm-r1070-7633"
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/crlone_lib="Gm-r1070"
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set of 9,216 clones

BASE COUNT	'OTHER EST'	SEAM LIBRARY	that is also listed under
235 a	171 c	113 g	223 t
ORIGIN			30 others

Query Match 7.6%; Score 163.4; DB 10; Length 772;
Best Local Similarity 52.7%;
Matches 326; Conservative 0.4; Wz=0.18e-35;

	1345	gtgtgtatcctgctgctgaatcgtgtaaactctctccaactctctgcctactctgctctgga	1404
aa			
ab	764	GAGTATNCCAAAGCGACANNNNNCNNAATTCACNNNNACATAGGGTNNNA	705
ay	1405	actcaggagctcaaatgctggctcaaacatcgaggctctgtgtaaaagagctttggcagg	1464
b	704	CGTATGGAGCTCAGATGTTGGCTTTAAATGATCAGGGGTATGCGAATTCATCTTTGGTACA	645
y	1465	caattggcgaagtccaagggaatgggggagtgtgggtatgttttgaaagccacgatctctgt	1524
	...	,	

Db	644	TGCACGAATGTTT	TAGACAAATGCAGCGTGC	GGTATGTG	AAAAANNCTG	AATTTCTTA	585		
Qy	1525	tgaaaaacttgctt	cttggtgtgcctt	caaacacacatcc	cagaaaaacacaccta	aa	1584		
Db	584	TTGAGAAAGGTCC	ACATAATGAGT	TTTTGATCTT	GAGAGAACATTC	CGCTGTG	GAAGAAA	525	
Qy	1585	tctcaagatcaa	agtttatga	ctacctgggt	gggacaagcctt	tccaaacgcatt	1644		
Db	524	CATTAAAGGT	AAAAAGTCTAT	ATGGGAC	TGGTGGAGCT	TAGATTT	CAGCCAAACAGACT	465	
Qy	1645	ttgacctattct	caactccagat	tttctcact	agggtgatt	tggtggagagtc	gtcgtg	1704	
Db	464	TTGATACT	TACTGCCACC	CAGATTTT	TATGTAAAGT	TTGATTT	TGTGGAGTTC	TGCTG	405
Qy	1705	acgaggccaagt	ggaagacat	ctgtggt	ggacaattc	atcaggcacc	ccattgggaatgag	1764	
Db	404	ATATGGCC	AAGAGAAAA	CAAGTGT	AAATCAAT	AAC	TGGTTTTCTGTT	TGGGATGAAG	345
Qy	1765	accatgagttt	gccctaaat	gacctagct	agctgc	actactgc	atcgcaggtccgagacc	1824	
Db	344	AGTTTGAT	TTCCCTTT	GACTGTTCC	AGAAC	TGCTTTG	TCGCGATAGATTC	CGAGAGA	285
Qy	1825	atgatgatgac	gaagatgatt	gaaggcagac	atgccttcc	catccatgaagtc	1884		
Db	284	ATGATAAGAG	TACAGAGGAT	GACTTTGGT	GGACAGACAT	GTTCCTGT	CTCAGAGCTAA	225	
Qy	1885	gggatgggtat	cgtgcatg	caaatgtac	gacaaagggc	aatgtact	gaaagcgctgc	1944	
Db	224	AATCTGGAT	CCGATCAG	TCCCCTCC	ATGATG	AAAGGGT	GACAAATTA	AAATCTGTGA	165
Qy	1945	tgatgttttc	atttca	1963					
Db	164	AGCTTTTGAT	GTGGTTCA	146					

RESULT 12

AL938235
LOCUS

DEFINITION

ACCESSION

VERSION
KEYWORDS

SOURCE ORGANISM

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL
COMMENT

100

1

Sun Jul 28 10:34:40 2002

[illegible]

Search completed: July 26, 2002, 14:51:57
Job time: 6241 sec

sequence 60, Appl
Sequence 3, Appl
Sequence 26, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 28, Appl
Sequence 28, Appl
Sequence 28, Appl
sequence 28, Appl
sequence 225, App
Sequence 2, Appl
Sequence 2, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 663, App
Sequence 14, Appl
Sequence 1, Appl
Sequence 1, Appl

ALIGNMENTS

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1
RESULT 1
US-08-138-641-1
; Sequence 1, Application US/08138641
; Patent No. 5474921
; GENERAL INFORMATION:
; APPLICANT: Koblan, Kenneth S.
; APPLICANT: Compilano, David L.
; TITLE OF INVENTION: ASSAY TO DETERMINE INHIBITORS OF
; TITLE OF INVENTION: PHOSPHINOISITIDE-SPECIFIC PHOSPHOLIPASE C-GAMMA
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Muthard
; STREET: P. O. Box 2000, 126 E. Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; CURRENT APPLICATION NUMBER: US/08/138.641

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APPLICATION NO: 100-138-641-1
 FILING DATE: 4/30/93
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Muthard, David A.
 REGISTRATION NUMBER: 35,297
 REFERENCE/DOCKET NUMBER: 18937
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (908) 594-3903
 TELEFAX: (908) 594-4720
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3870 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cdna

Query Match 4.6%; Score 97.6; DB 1; Length 3870;
Best Local Similarity 51.9%; pred. No. 3.5e-20;
Matches 220; Conservative 0; Mismatches 204; Indels 0; Caps 0;

DY
db

436 agacatgacgcagccgatgtcgcactatttcataatcaccg998
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959 AACCATGAACAACCACACTGTCCTCACTATTGGATCTCTCCTCGCATATACGTATCTGA 1018

959 AAACCATGAACAACCCACTGTCACATATGGGACATCTT

GenCore version 4.5
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rate search using sw model

run on: July 26, 2002, 14:05:57 ; Search time 68.43 seconds
(without alignments)
7678.066 Million cell updates/sec

Title: US-09-828-447-7
 Perfect score: 2139
 Sequence: 1 atccgggcttcgggagtt.....gtgcaccaagtttaacgcc 2139

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues
Parameters: 767066

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%

listing first 45 summaries

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6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, Σ is the sum of the total score distribution.

SUMMARIES

result No.	Score	Query		ID	Description
		Match	Length		
1	97.6	4.6	3870	1	US-08-138-641-1
2	97.6	4.6	3870	1	US-08-138-133-1
3	97.6	4.6	3893	1	US-08-138-641-3
4	97.6	4.6	3893	1	US-08-138-133-3
5	56.4	2.6	434	4	US-09-677-064-27
6	56.4	2.6	434	4	US-09-677-064-27
7	53	2.5	7218	1	US-08-232-463-14
8	42.2	2.0	11717	1	US-08-801-263A-4
9	42.2	2.0	11717	3	US-09-102-248-4
10	40.6	1.9	11663	1	US-08-446-932-1
11	40.6	1.9	11663	1	US-08-801-263A-1
12	40.6	1.9	11663	3	US-08-801-263A-7
13	40.6	1.9	11663	3	US-09-102-248-1
14	40.6	1.9	11663	3	US-09-102-248-7
15	39.2	1.8	11703	1	US-08-801-263A-8
16	39.2	1.8	11703	3	US-09-102-248-8
17	39.2	1.8	13905	4	US-08-972-218-1
18	39.2	1.8	16656	1	US-08-741-881-1
19	39.2	1.8	16656	2	US-08-739-158-1
20	39.2	1.8	16656	2	US-08-739-167-1
21	39.2	1.8	16656	3	US-08-404-796-1
22	39.2	1.8	16656	3	US-08-931-869-1
23	39.2	1.8	16656	4	US-09-350-399-1
24	35.6	1.7	752	6	US-055030-12
25	35.6	1.7	8298	5	PCT-US93-03076-1
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27	34.4	1.6	1460	2	US-08-933-750C-60


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; SEQUENCE CHARACTERISTICS:
; LENGTH: 3893 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-138-641-3

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Query Match          4.6%; Score 97.6; DB 1; Length 3893;
Best Local Similarity 51.9%; Pred. No. 3.5e-20;
Matches 220; Conservative 0; Mismatches 204; Indels 0; Gaps 0;

QY 436 aagacatgacgacgagcgtgctgcaactatttcattacacggccataactcgtacatga 495
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Db 959 AAACCATGAACAACCCACTGTCTCACTATTGGATCTCTTCTCCGCAATAACGTATCTGA 1018

QY 496 ccggcaaccagctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 555
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Db 1019 CTGGGACCAAGTCTCCAGCGAGTCTCTCCCTGGAAGCTTACGCTCGCTGAGGATGG 1078

QY 556 gctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 615
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Db 1079 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1138

QY 616 acggaacacacttaccatcccggtgctgtcccaaaagtgtcacagccatcaagaata 675
    || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| || |||||
Db 1139 ATGGGCACACCTCACCACCAAGATTAAAGTTCTCAGATGCTCTGCGACACCATCAAGGAGC 1198

QY 676 acgctcttcacctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 735
    || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| || |||||
Db 1199 ACGGTTCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 1258

QY 736 aattacagggccatgctgcagagatttttagacaaattctcgcagagcgcctgtattac 795
    || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| || |||||
Db 1259 CCCAGAGAGGACATGCCCCAGCACTTCAGGAAGGTGCTCGGTGACACGCTCCTCACCA 1318

QY 796 caccacacacatgcatgattgtagtgccttcacccgagtcactcaagagaagataca 855
    || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| || |||||
Db 1319 AGCCGTGGACATGTCGGCTGATGGGCTCCCTTCTCCCAACCAAGCTCAAGAGGAATCC 1378

QY 856 taat 859
Db 1379 TGAT 1382

```

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RESULT 4
US-08-138-133-3
; Sequence 3, Application US/08138133
; Patent No. 5519163
; GENERAL INFORMATION:
; APPLICANT: GIBBS, JACKSON B.
; APPLICANT: KOBLEN, KENNETH S.
; APPLICANT: MACLEOD, ANGUS M.
; APPLICANT: MERCHANT, KEVIN J.
; TITLE OF INVENTION: INHIBITORS OF PHOSPHOINOSITIDE-SPECIFIC
; TITLE OF INVENTION: PHOSPHOLIPASE C
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID A. MUTHARD
; STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: U.S.A.
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/138,133
; FILING DATE:

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; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MUTHARD, DAVID A.
; REGISTRATION NUMBER: 35,297
; REFERENCE/DOCKET NUMBER: 18938
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-3903
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3893 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-138-133-3

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Query Match          4.6%; Score 97.6; DB 1; Length 3893;
Best Local Similarity 51.9%; Pred. No. 3.5e-20;
Matches 220; Conservative 0; Mismatches 204; Indels 0; Gaps 0;

QY 436 aagacatgacgacgagcgtgctgcaactatttcattacacggccataactcgtacatga 495
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Db 959 AAACCATGAACAACCCACTGTCTCACTATTGGATCTCTTCTCCGCAATAACGTATCTGA 1018

QY 496 ccggcaaccagctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 555
    || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| || |||||
Db 1019 CTGGGACCAAGTCTCCAGCGAGTCTCTCCCTGGAAGCTTACGCTCGCTGAGGATGG 1078

QY 556 gctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 615
    || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| || |||||
Db 1079 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1138

QY 616 acggaacacacacttaccatcccggtgctgtcccaaaagtgtcacagccatcaagaata 675
    || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| || |||||
Db 1139 ATGGGCACACCTCACCACCAAGATTAAAGTTCTCAGATGCTCTGCGACACCATCAAGGAGC 1198

QY 676 acgctcttcacctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 735
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Db 1199 ACGGTTCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 1258

QY 736 aattacagggccatgctgcagagatttttagacaaattctcgcagagcgcctgtattac 795
    || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| || |||||
Db 1259 CCCAGAGAGGACATGCCCCAGCACTTCAGGAAGGTGCTCGGTGACACGCTCCTCACCA 1318

QY 796 caccacacacatgcatgattgtagtgccttcacccgagtcactcaagagaagataca 855
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Db 1319 AGCCGTGGACATGTCGGCTGATGGGCTCCCTTCTCCCAACCAAGCTCAAGAGGAATCC 1378

QY 856 taat 859
Db 1379 TGAT 1382

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RESULT 5
US-09-118-442-27
; Sequence 27, Application US/09118442B
; Patent No. 6197561
; GENERAL INFORMATION:
; APPLICANT: Martino-Catt, Susan J.
; APPLICANT: Wang, Hongyu
; APPLICANT: Beach, Larry R.
; APPLICANT: Wang, Xun
; APPLICANT: Bowen, Benjamin A.
; TITLE OF INVENTION: Genes Controlling Phytate Metabolism in
; TITLE OF INVENTION: Plants and Uses Thereof
; FILE REFERENCE: 0706
; CURRENT APPLICATION NUMBER: US/09/118,442B
; CURRENT FILING DATE: 1998-07-17
; EARLIER APPLICATION NUMBER: 60/055,446
; EARLIER FILING DATE: 1997-08-11
; EARLIER APPLICATION NUMBER: 60/055,526

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; EARLIER FILING DATE: 1997-08-08
; EARLIER APPLICATION NUMBER: 60/053,944
; EARLIER FILING DATE: 1997-07-28
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 434
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(434)
; OTHER INFORMATION: n = A,T,C or G
US-09-118-442-27

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Query Match      2.6%; Score 56.4; DB 4; Length 434;
Best Local Similarity 57.0%; Pred. No. 7.7e-08;
Matches 102; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

Qy 1613 gggatgggacaaggccttttccaaacgccatttttgacattattccacctccagattctt 1672
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Db 105 gggtgnggcattggacttcagtaaaactcattcgatgccttttcctccagattctta 164
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 1673 cactaggggtgatttggtgggagtgacctgctgacagagcccaagtggaaagacactctgtgt 1732
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 165 tactaggggtaggatcgcaaggtgtgaagcgacacagtgatgaagaagacaaagggtgat 224

Qy 1733 ggacaattcatgggcacccccattggaaatgaggaccattgatttgcctaaaatgcctgt 1791
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 225 taaggaccactcagttaccatattcagatgagaagattcagctctctctcdaacaggttccg 283
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>>> RESULT 6
>>> US-09-677-064-27
>>> Sequence 27, Application US/09677064
>>> Patent No. 6291224
>>> GENERAL INFORMATION:
>>> APPLICANT: Martino-Catt, Susan J.
>>> APPLICANT: Wang, Hongyu
>>> APPLICANT: Beach, Larry R.
>>> TITLE OF INVENTION: Genes Controlling
>>> TITLE OF INVENTION: Plants and Uses
>>> FILE REFERENCE: 0706D
>>> CURRENT APPLICATION NUMBER: US/09/677-064-27
>>> CURRENT FILING DATE: 2000-09-29
>>> PRIOR APPLICATION NUMBER: 60/055,414
>>> PRIOR FILING DATE: 1997-08-11
>>> PRIOR APPLICATION NUMBER: 60/055,514
>>> PRIOR FILING DATE: 1997-08-08
>>> PRIOR APPLICATION NUMBER: 60/053,919
>>> PRIOR FILING DATE: 1997-07-28
>>> PRIOR APPLICATION NUMBER: 09/118,417
>>> PRIOR FILING DATE: 1998-07-17
>>> NUMBER OF SEQ ID NOS: 31
>>> SOFTWARE: FastSeq for Windows Vers
>>> SEQ ID NO 27
>>> LENGTH: 434
>>> TYPE: DNA
>>> ORGANISM: Zea mays
>>> FEATURE:
>>> NAME/KEY: misc_feature
>>> LOCATION: (1)...(434)
>>> OTHER INFORMATION: n = A,T,C or G
>>> US-09-677-064-27

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Query Match      2.6%; Score 56.4; DB 4; Length 434;
Best Local Similarity 57.0%; Pred. No. 7.7e-08;
Matches 102; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

Qy 1613 gggatgggacaaggcctttccaaagcgcatttgacctattctcaactccagattttt 1672
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Db	105	gggtgngccaatggacttcagtaaaactcatttgcgatccttttcgctccagatttcta	164
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Db	165	tactagggtgaggtatcgacaggttgaagcagcacagctgtgtagaagaaagacaaaggttgat	224
Qy	1733	ggacaattcatggtgacccccatttgggaatgagacacattgatttgcctcaaatgcccctg	1791
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RESULT 7
US-08-232-463-14/c
; Sequence 14, Application US/082322463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: ptzgpt-Fts
; JUS-08-232-463-14

[illegible]

us-09-828-447-7.rni

Sun Jul 28 10:34:38 2002

QY 133 tagcatgttgcgaagtgaaacccggaaggggagcagacacgtgtgtggggagg 192
 Db 1201 RRR 1142
 QY 193 tgttcaataatagcagagagatgagtgagtgaggggtgtgtgaaatttgc 252
 Db 1141 RRR 1082
 QY 253 atacagagcaagggatgtcgacttacccttgatgacgccaagc 297
 Db 1081 RRR 1037

RESULT 8
 US-08-801-263A-4
 ; Sequence 4, Application US/08801263A
 ; Patent No. 5811407
 ; GENERAL INFORMATION:
 ; APPLICANT: Johnston, Robert E.
 ; APPLICANT: Davis, Nancy L.
 ; APPLICANT: Simpson, Dennis A.
 ; TITLE OF INVENTION: System for the In Vivo Delivery and
 ; Expression of Heterologous Genes in the Bone Marrow
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Bell Seltzer Park & Gibson, P.A.
 ; STREET: 1211 East Morehead Street
 ; CITY: Charlotte
 ; STATE: No. 5811407th Carolina
 ; COUNTRY: USA
 ; ZIP: 28234
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/801.263A
 ; FILING DATE: 19-FEB-1997
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Sibley, Kenneth D.
 ; REGISTRATION NUMBER: 31,665
 ; REFERENCE/DOCKET NUMBER: 5470-147
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 919-420-2200
 ; TELEFAX: 919-881-3175
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1171 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; US-08-801-263A-4

Query Match 2.0%; Score 42.2; DB 1; Length 1171;
 Best Local Similarity 54.1%; Pred. No. 0.019;
 Matches 86; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
 QY 826 cttcaccggagtcactgaagagagatcataatctccaccacccgcaagagatc 885
 Db 1438 CTTTGCCCATGCTGCTGAGCGAGAGATAAATTGGCAATTACAACCAAGAGGAGAA 1497
 QY 886 tcgaagcatgttccacgcagcaaaattggccatgagagacaggaattctgtgagagcttg 945
 Db 1498 AACTGCTGCAAGTCCCGGAGGAATAGTCATCGAGGCCCAAGGCTCTTTCGAGGATGCTC 1557
 QY 946 agaaggaagacaaattggagcagacacacattcgtccccc 984
 Db 1558 AGGAGGAATCCAGAGCGGAGAGAGCTCCGAGAGCACTCC 1596

RESULT 9
 US-09-102-248-4
 ; Sequence 4, Application US/09102248
 ; Patent No. 6008035
 ; GENERAL INFORMATION:
 ; APPLICANT: Johnston, Robert E.
 ; APPLICANT: Davis, Nancy L.
 ; APPLICANT: Simpson, Dennis A.
 ; TITLE OF INVENTION: System for the In Vivo Delivery and
 ; Expression of Heterologous Genes in the Bone Marrow
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Bell Seltzer Park & Gibson, P.A.
 ; STREET: 1211 East Morehead Street
 ; CITY: Charlotte
 ; STATE: No. 6008035th Carolina
 ; COUNTRY: USA
 ; ZIP: 28234
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/102.248
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION NUMBER: US 08/801.263
 ; FILING DATE: 19-FEB-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Sibley, Kenneth D.
 ; REGISTRATION NUMBER: 31,665
 ; REFERENCE/DOCKET NUMBER: 5470-147
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 919-420-2200
 ; TELEFAX: 919-881-3175
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1171 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; US-09-102-248-4

Query Match 2.0%; Score 42.2; DB 3; Length 1171;
 Best Local Similarity 54.1%; Pred. No. 0.019;
 Matches 86; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
 QY 826 cttcaccggagtcactgaagagagatcataatctccaccacccgcaagagatc 885
 Db 1438 CTTTGCCCATGCTGCTGAGCGAGAGATAAATTGGCAATTACAACCAAGAGGAGAA 1497
 QY 886 tcgaagcatgttccacgcagcaaaattggccatgagagacaggaattctgtgagagcttg 945
 Db 1498 AACTGCTGCAAGTCCCGGAGGAATAGTCATCGAGGCCCAAGGCTCTTTCGAGGATGCTC 1557
 QY 946 agaaggaagacaaattggagcagacacacattcgtccccc 984
 Db 1558 AGGAGGAATCCAGAGCGGAGAGAGCTCCGAGAGCACTCC 1596

RESULT 10
 US-08-446-932-1
 ; Sequence 1, Application US/08446932
 ; Patent No. 5639650
 ; GENERAL INFORMATION:
 ; APPLICANT: Johnston, Robert E.
 ; APPLICANT: Simpson, Dennis
 ; APPLICANT: Davis, Nancy L.

COMPUTER READABLE FORM: _____
MEDIUM TYPE: _____ Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS
SOFTWARE: PatentL Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: DUS/08/801,263A
APPLICATION NUMBER: _____
FILING DATE: 19-FEB-1997

ATTORNEY/AGENT INFORMATION: 314
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5470-147
TELECOMMUNICATION INFORMATION:
TELEPHONE: 913-420-2200
TELEFAX: 913-420-2200

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DEFINITION: 919-881-3175
SEQUENCE INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
    LENGTH: 11663 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: double
    TOPOLOGY: linear
    MOLECULE TYPE: cDNA
    FEATURE:
        NAME/KEY: CDS

```

LOCATION:	60..7559	
FEATURE:		
NAME/KEY:	CDS	
LOCATION:	7608..11342	
	801-263A-1	
y Match	1.9%	Score 40.6; DB 1;
Local Similarity	53.5%	DB 2;

	QY	826	cttcaccggagctca	ctgaaggaagatcata	atctccacc	aaacccgcgaaggagt	atc	885	
	Db	1438	CTTTGCCCATCT	CGCTGAGG	CAGACAT	GAATGTCAT	TCAACCAAGAGGAGG	AAA	1497
	QY	886	tcgaagcatgtt	ccacgcagaaattg	cccatggagaa	caggaaatctg	gtggagagcttg	945	
	Db	1498	AACGTCTCAAG	TCCCGAGGAAAT	TAGTTATG	GAGGCCAAG	GCTGCTTTCGAGAT	GCTC	1557
	QY	946	agaaggagaaca	aatggagcagacc	aatctcgctcccc	984			
	Db	1558	AGGAGGAATC	CAGAGCGGAGA	AGCTCCGAGAG	CACTCC	1596		

GEN. NO. 5811407
 GENERAL INFORMATION:
 APPLICANT: Johnston, Robert E.
 APPLICANT: Davis, Nancy L.
 APPLICANT: Simpson, Dennis A.
 TITLE OF INVENTION: System for the In Vivo Delivery and
 TITLE OF INVENTION: Expression of Heterologous Genes in the Bone Marrow
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Bell Seltzer Park & Gibson, P.A.
 STREET: 1211 East Morehead Street
 CITY: Charlotte
 STATE: No. 5811407th Carolina
 COUNTRY: USA
 ZIP: 28234
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA.

SUMMARIES

ALIGNMENTS

PA (BADI) BASF PLANT SCI GMBH.

PI	Costa Silva EO, Bohnert HJ, Van Thienen N, Chen R, Ishitani M;
XX	WPI; 2002-049152/06.
DR	P-PSDB; AAU11620.
DR	
XX	
PT	New polypeptide, useful for increasing tolerance to environmental
PT	stress, comprises a Signal Transduction Stress-Related Protein selected
PT	from phospholipases, 14-3-3 proteins and calcium binding proteins
XX	
XX	Claim 4; Fig 2B; 101pp; English.
XX	
CC	The invention relates to a Signal Transduction Stress-Related Protein
CC	(STSRP) isolated from <i>Physcomitrella patens</i> , and selected from
CC	Phospholipase C (PLC)-1 protein, PLC-2 protein, 14-3-3 protein
CC	(14-3-3P)-1, 14-3-3P-2 and Ca ²⁺ -Binding Protein (CBP)-1, or their
CC	orthologues. Also include are a transgenic plant transformed with
CC	an STSRP coding nucleic acid, where the expression of the nucleic acid in
CC	the plant cell results in increased tolerance to an environmental stress
CC	as compared to a wild type variety of the plant cell, a nucleic
CC	acid encoding an STSRP, and an expression vector comprising the nucleic
CC	acid. The STSRP and nucleic acids are useful for increasing tolerance to
CC	acid. The STSRP and nucleic acids are useful for increasing tolerance to
CC	environmental stress selected from salinity, drought and low temperature,
CC	in transgenic plants including monocot and dicot selected from maize,
CC	wheat, rye, oat, triticale, rice, barley, soybean, peanut, cotton,
CC	rapieseed, canola, manihot, pepper, sunflower, tagetes, solanaceous
CC	plants, potato, tobacco, eggplant, tomato, <i>Vicia</i> species, pea, alfalfa,
CC	coffee, cacao, tea, <i>Salix</i> species, oil palm, coconut, perennial grass and
CC	forage crops. The nucleic acid is also useful for identifying organisms
CC	e.g. <i>Physcomitrella patens</i> in a mixed population of microorganisms,
CC	for evolutionary and protein structural studies and are useful as markers
CC	for specific regions of the genome. The present sequence encodes PLC-2.
XX	
XX	Sequence 2139 bp: 588 A: 497 C: 564 G: 490 T: 0 other:

[illegible][illegible]

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Qy	1721	gacatctggtggacaattcatgggcccacccattggaatgagaccatgagtttgcct	1780
Db	1794	aacttcggttagatgacgttttggaaacccactggagcaggtacacaggttttaacct	1853
Qy	1781	aaatgcccctgagctgcacactacttcgcatcgaggtccgagacatgatgatgacgaa	1840
Db	1854	taaatgcccctgagctgcacactctccgaattgaattgagatcacgacgagaaagtca	1913
Qy	1841	agatgagtttgaaggcagacatgccttcccatccatcgaatccggtatgggtatcggtg	1900
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Db	2034	tcaaaa 2039	
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ID	AA	SI7961 standard; CDNA; 706 BP.	
XX	XX	AA	SI7961;
XX	XX	12-MAR-2002 (first entry)	
XX	XX	P. patens STSRP protein, PLC-2, partial CDNA.	
XX	XX	Signal transduction stress-related protein; STSRP; PLC-1; PLC-2;	
KW	KW	14-3-3P-1; 14-3-3P-2; CBP-1; phospholipase C; Ca2+ binding protein;	
KW	KW	transgenic plant; environmental stress; salinity; drought;	
KW	KW	low temperature; ss.	
XX	XX	Physcomitrella patens.	
OS	OS	WO200177355-A2.	
XX	XX	18-OCT-2001.	
XX	XX	06-APR-2001; 2001WO-US11398.	
XX	XX	07-APR-2000; 2000US-196001P.	
XX	XX	(BADI) BASF PLANT SCI GMBH.	
XX	XX	Costa Silva EO, Bohnert HJ, Van Thiel N, Chen R, Ishitani M;	
XX	XX	WPI; 2002-049152/06.	
XX	XX	New polypeptide, useful for increasing tolerance to environmental	
XX	XX	stress, comprises a Signal transduction Stress-Related Protein selected	
XX	XX	from phospholipases, 14-3-3 proteins and calcium binding proteins -	
XX	XX	Example 5; Fig 1B; 101pp; English.	
XX	XX	The invention relates to a Signal Transduction Stress-Related Protein	
XX	XX	(STSRP) isolated from Physcomitrella patens, and selected from	
XX	XX	Phospholipase C (PLC)-1 protein, PLC-2 protein, 14-3-3 protein	
XX	XX	(14-3-3P)-1, 14-3-3P-2 and Ca2+-binding Protein (CBP)-1, or their	
XX	XX	orthologues. Also include are a transgenic plant transformed with	
XX	XX	an STSRP coding nucleic acid, where the expression of the nucleic acid in	
XX	XX	the plant cell results in increased tolerance to an environmental stress	
XX	XX	as compared to a wild type variety of the plant cell, a nucleic	

[illegible]

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Qy	334	c---cttcggactgcgctctatacaactcagactctgtcgaagagagcgcttttcggaagtact	390	9905-01300445 9905-01303449 9905-01305100 9905-01308911 9905-01314449 9905-01320448 9905-01324047 9905-01324484 9905-01324845 9905-01324886 9905-01324887 9905-01328633 9905-01342556 9905-01342818 9905-01342919 9905-01342211 9905-01343700 9905-01343768 9905-01349411 9905-01351244 9905-01353533 9905-01356249 9905-01360211 9905-01363921 9905-01367822 9905-01372222 9905-01375228 9905-01375021 9905-01377241 9905-01380944 9905-01385400 9905-01388477 9905-01391452 9905-01394557 9905-01394577 9905-01394588 9905-01394589 9905-01394600 9905-01394611 9905-01394622 9905-01394633 9905-01397500 9905-01397633 9905-01398177 9905-01398919 9905-01403533 9905-01403544 9905-01403544 9905-01403544 9905-01406953 9905-01408223 9905-01409911 9905-01412877 9905-01418422 9905-01421544 9905-01420555 9905-01423900 9905-01428033 9905-01429200 9905-01429777 9905-01435422 9905-01436244 9905-01440055 9905-01440855 9905-01440866 9905-01443255 9905-01443311 9905-01443332
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Qy	746	ccatgtgtcagagatttttagagcaaatctcggagacgcccctgtattatccaccaccaac	805
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XX	DT	08-FEB-2001 (first entry)	
XX	XX	Human ORFX ORF1967 polynucleotide sequence SEQ ID NO:3933.	
XX	DE	Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;	
XX	KW	vulnary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;	
XX	KW	anticonvulsant; osteopathic; antiarthritis; immunosuppressant; cardiac;	
XX	KW	immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;	
XX	KW	hypotensive; dermatological; immunosuppressive; antiinflammatory;	
XX	KW	antiviral; antibacterial; antifungal; antirheumatic; antithyroid;	
XX	KW	antianemic; gene therapy; cancer; proliferative disorder; hypertension;	
XX	KW	neurodegenerative disorder; osteoarthritis; graft vs host disease;	
XX	KW	cardiovascular disease; diabetes mellitus; hypothyroidism; AIDS;	
XX	KW	cholesterol ester storage; systemic lupus erythematosus; infection;	
XX	KW	severe combined immunodeficiency; malaria; autoimmune disorder; asthma;	
XX	KW	allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;	
XX	KW	bone damage; cartilage damage; antiinflammatory disease; coagulation;	
XX	KW	thrombosis; contraceptive; ss.	
XX	OS	Homo sapiens.	
XX	XX	WO200058473-A2.	
XX	PN	05-OCT-2000.	
XX	PD	31-MAR-2000; 2000WO-US08621.	
XX	PF	31-MAR-1999; 99US-0127607.	
XX	PR	02-APR-1999; 99US-0127636.	
XX	PR	05-APR-1999; 99US-0127728.	
XX	PR	30-MAR-2000; 2000US-0540763.	
XX	XX	(CURA-) CURAGEN CORP.	
XX	XX	Shimkets RA, Leach M;	
XX	XX	WPI; 2000-602362/57.	
XX	XX	P-PSDB; AAB42203.	
XX	XX	Novel nucleic acids and peptides derived from open reading frame X,	
XX	PT	useful for treating e.g. cancers, proliferative disorders,	
XX	PT	neurodegenerative disorders and cardiovascular disease -	
XX	XX		

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XX	AC	ABL07327;	
XX	DT	26-MAR-2002 (first entry)	
XX	XX	Drosophila melanogaster expressed polynucleotide SEQ ID NO 16463.	
XX	DE	Drosophila; developmental biology; cell signalling; insecticide;	
XX	KW	pharmaceutical; gene; ss.	
XX	OS	Drosophila melanogaster.	
XX	XX	WO200171042-A2.	
XX	PN	27-SEP-2001.	
XX	PD	23-MAR-2001; 2001WO-US09231.	
XX	PF	23-MAR-2000; 2000US-191637P.	
XX	PR	11-JUL-2000; 2000US-0614150.	
XX	PR	(PEKE) PE CORP NY.	
XX	PA	Venter JC, Adams M, Li PWD, Myers EW;	
XX	PI	WPI; 2001-656860/75.	
XX	XX	P-PSDB; ABB63224.	
XX	DR	New isolated nucleic acid detection reagent for detecting 1000 or more	
XX	DR	genes from Drosophila and for elucidating cell signalling and cell-cell	
XX	PT	interactions -	
XX	PT	Claim 1; SEQ ID NO 16463; 21pp + Sequence Listing; English.	
XX	PS	The invention relates to an isolated nucleic acid detection reagent	
XX	CC	capable of detecting 1000 or more genes from Drosophila. The invention is	
XX	CC	useful in developmental biology and in elucidating cell signalling and	
XX	CC	cell-cell interactions in higher eukaryotes for the development of	
XX	CC	insecticides, therapeutics and pharmaceutical drugs. The invention	
XX	CC	discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA	
XX	CC	sequences (ABL01840-ABL16175) and the encoded proteins	
XX	CC	(ABB57737-ABB72072).	
XX	CC	The sequence data for this patent did not form part of the printed	
XX	CC	specification, but was obtained in electronic format directly from WIPO	
XX	CC	at ftp.wipo.int/pub/published_pct_sequences.	
XX	XX	Sequence 5751 BP; 1605 A; 1257 C; 1329 G; 1560 T; 0 other;	
XX	SQ		
Query Match	3.7%;	Score 78.4; DB 23; Length 5751;	
Best Local Similarity	47.2%;	Pred. NO. 2.9e-13;	
Matches 238; Conservative	0;	Mismatches 266; Indels 0; Gaps 0;	
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Qy	446	gcagccgagtgatgcactatttatttcacggcgccataactcgtacgtgacggcgaacca	505
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Qy	506	gctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc	565
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Qy	566	tgtggaattggaactgttggtcgtgatgacaaagcgcgatgaagggtcacacacaggaacac	625

QY	436	aagacatgacgcagcgcgatgtgcgactatttcattatcacggggccataaactcgtaacctga	495
Db	6382	aagaactgcagctaccctctcaatactatcatcgaaatttgcgcaaatcacctacctca	6441
QY	496	cgggcacacagctgacgcagcagacgcagcagcacacccatcgctggcggaactgcggcgcg	555

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 26, 2002, 13:34:42 ; Search time 3923.35 Seconds
(without alignments)
11409.092 Million cell updates/sec

Title: US-09-828-447-7

Perfect score: 2139

Sequence: 1 atcccggttcgaggttt.....gtgacccaaggttaacgcc 2139

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: gb_ba:*

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5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

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9: gb_pr:*

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11: gb_sts:*

12: gb_sv:*

13: gb_un:*

14: gb_vi:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_on:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_to:*

27: em_sts:*

28: em_un:*

29: em_vi:*

30: em_htg_hum:*

31: em_htg_inv:*

32: em_htg_other:*

33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description

1	2139	100.0	2139	6	AX2811101	AX2811101 Sequence
2	841.6	39.3	2276	6	AX2811100	AX2811100 Sequence
3	546.2	25.5	706	6	AX281096	AX281096 Sequence
4	422	19.7	760	6	AX281095	AX281095 Sequence
5	283.8	13.3	2134	8	GMU41474	U41474 Glycine max
6	280.2	13.1	2079	8	GMU25027	U25027 Glycine max
7	258.4	12.1	2113	8	PSPLC	Y15253 Pisum sativ
8	254	11.9	1776	8	AY053422	AY053422 Arabidops
9	249.4	11.7	2038	8	DS291467	AY291467 Digitaria
10	247.6	11.6	1894	8	GMU41473	U41473 Glycine max
11	243.4	11.4	1746	8	AF108123	AF108123 Brassica
12	240.2	11.2	2170	8	GMU41475	U41475 Glycine max
13	233.4	10.9	2207	8	AF332874	AF332874 Oryza sat
14	229.4	10.7	2066	8	NRPHOSLPC	X95877 N.rustica m
15	224.6	10.5	2013	8	NRPHOSLPC	X95877 N.rustica m
16	221.4	10.4	1981	8	STPLCIGEN	Y11931 N.rustica m
17	218.6	10.2	1746	8	AY040054	X93564 S.tuberosum
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30	109.2	5.1	4344	4	BTPLCII	Y00301 Bovine mRNa
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ALIGNMENTS

RESULT 1

AX2811101 LOCUS
DEFINITION Sequence 7 from Patent WO0177355.
ACCESSION AX2811101
VERSION AX2811101.1 GI:16608368
KEYWORDS
SOURCE Physcomitrella patens.
ORGANISM Physcomitrella patens.

REFERENCE 1 (sites)
AUTHORS costa e Silva,O.D., Bohnert,H.J., van Thielens,N., Chen,R. and Ishitani,M.
TITLE Signal transduction stress-related proteins and methods of use in
JOURNAL Plants
FEATURES BASF Plant Science GmbH (DE)
source Location/Qualifiers
1..2139 /organism="Physcomitrella patens"
/db_xref="taxon:3218" 490 t

BASE COUNT 588 a 437 c 564 g 490 t

ORIGIN

Query Match 100.0%; Score 2139; DB 6; Length 2139;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2139; Conservative 0; Mismatches 0; Gaps 0;

QY 1 atccccggcttcggagtttaagggatgtcacggcgtggaagacgagggcggtgatgca 60
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RESULT 2
 AX281100
 LOCUS AX281100 2276 bp DNA linear PAT 02-NOV-2001
 DEFINITION Sequence 6 from Patent WO0177355.
 ACCESSION AX281100
 VERSION AX281100.1 GI:16608367
 KEYWORDS
 SOURCE
 ORGANISM
 Physcomitrella patens.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
 Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
 1 (sites)
 costa e Silva, O.D., Bohnert, H.J., van Thielens, N., Chen, R. and
 Ishitani, M.
 TITLE Signal transduction stress-related proteins and methods of use in
 Plants
 JOURNAL Patent: WO 0177355-A 6 18-OCT-2001;
 BASF Plant Science GmbH (DE)
 FEATURES
 source
 BASE COUNT 626 a 481 c 609 g 560 t
 ORIGIN

Query Match 39.3%; Score 841.6; DB 6; Length 2276;
 Best Local Similarity 67.7%; Pred. No. 4.8e-246;
 Matches 1304; Conservative 0; Mismatches 524; Indels 98; Gaps 5;

QY 80 gtgcacgagtgtaagggatcggtcgctgcactgggttgcaaaatgtgtccatagcatg 139
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QY 140 ttgtcgaagtggaaaccccggaagggatccgagcaagacctggtggggaggtgttca 199
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RESULT 4
AX281095 AX281095 760 bp DNA linear PAT 02-NOV-2001
LOCUS
DEFINITION Sequence 1 from Patent WO0177355.
ACCESSION AX281095
VERSION AX281095.1 GI:16608362
KEYWORDS
SOURCE Physcomitrella patens.
ORGANISM Physcomitrella patens
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
REFERENCE 1 (sites)
AUTHORS Costa e Silva, O.D., Bohnert, H.J., van Thiel, N., Chen, R. and
Ishitani, M.
TITLE Signal transduction stress-related proteins and methods of use in
plants
JOURNAL Patent: WO 0177355-A 1 18-OCT-2001;
BASF Plant Science GmbH (DE)
FEATURES
Location/Qualifiers
Source
1..760
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BASE COUNT 198 a 178 c 201 g 183 t
ORIGIN

Query Match 19.7%; Score 422; DB 6; Length 760;
Best Local Similarity 74.0%; Pred. No. 1.6e-117;
Matches 549; Conservative 0; Mismatches 190; Indels 3; Gaps 1;

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RESULT 3
AX281096 AX281096 706 bp DNA linear PAT 02-NOV-2001
LOCUS
DEFINITION Sequence 2 from Patent WO0177355.
ACCESSION AX281096
VERSION AX281096.1 GI:16608363
KEYWORDS
SOURCE Physcomitrella patens.
ORGANISM Physcomitrella patens
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
REFERENCE 1 (sites)
AUTHORS Costa e Silva, O.D., Bohnert, H.J., van Thiel, N., Chen, R. and
Ishitani, M.
TITLE Signal transduction stress-related proteins and methods of use in
plants
JOURNAL Patent: WO 0177355-A 2 18-OCT-2001;
BASF Plant Science GmbH (DE)
FEATURES
Location/Qualifiers
Source
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BASE COUNT 220 a 181 c 171 g 133 t 1 others
ORIGIN

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Best Local Similarity 95.9%; Pred. No. 1.3e-155;
Matches 636; Conservative 0; Mismatches 18; Indels 9; Gaps 7;

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DB 68 TGTCAGCCATCCAGAAATACGCTTCTTCACTCGAGTACCAGTTTGGTTACTAT 127
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Sun Jul 28 10:34:38 2002

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7 JUL 1954

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DEFINITION	Y15253				
ACCESSION	Y15253.1 GI:2584805				
VERSION	phospholipase C; PLC gene.				
KEYWORDS	Pisum				
SOURCE	Pisum sativum				
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eustosids I; Fabales; Fabaceae; Papilionoideae; Viciae;				
	Pisum.				
REFERENCE	1 (bases 1 to 2113)				
AUTHORS	Venkataraman,G., Reddy,M.K. and Sopory,S.K.				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 2113)				
AUTHORS	Reddy,M.K.				
TITLE	Direct Submission				
JOURNAL	Submitted (27-OCT-1997) M.K. Reddy, International Centre for Genetic Engineering and Biotechnology, Plant Molecular Biology Lab, Aruna Asaf Ali Marg, New Delhi - 110 067, INDIA				
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BASE COUNT					
ORIGIN					

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 LOCUS Arabidopsis thaliana phospholipase C4
 DEFINITION (PLC4) mRNA, complete cds.

ACCESSION AY053422
 VERSION AY053422.1 GI:16555230

KEYWORDS
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ORGANISM

Arabidopsis thaliana
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 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

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LOCUS
2038 bp mRNA linear PLN 18-OCT-2000
Digitalis sanguinalis mRNA for phosphoinositide-specific
phospholipase C (plc2 gene).

REFERENCE

1 (bases 1 to 2038)

Claude, J., Vidal, J., and Grisvard, J.

JOURNAL
TITLE Direct Submission
Submitted (11-OCT-2000) Coursol S., Université Paris XI, Institut
de Biotechnologie des Plantes, UMR 8618, 91405, Orsay Cedex, FRANCE

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DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

[illegible]

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DEFINITION complete cds.
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Glycine.
1 (bases 1 to 2170)
Shi,J., Gonzales,R.A. and Bhattacharya,M.K.
Phosphoinositide-specific phospholipase Cs contain a C-terminal
domain having homology to the C2 domain of protein kinase C
Unpublished
2 (bases 1 to 2170)
Clouse,J.A.
Direct Submission
Submitted (29-NOV-1995) Joe A. Clouse, The Samuel Roberts Noble
Foundation Inc., Plant Biology Division, P.O. Box 2180, Ardmore,
OK 73402, USA
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QY 606 aaggtcacacgcggaacacaccttaccaatcccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 665
DB 467 GATGCTTCTTCATGGAAGCACTTTGACCTTCTCTGCGACATCAATATCTCTGAGTCT 526

-----LAKHAGVKVIELIWPNS

100

Sun Jul 28 10:34:38 2002

ORGANISM	Nicotiana rustica
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
AUTHORS	Pical, C., Kopka, J., Muller-Rober, B., Hetherington, A.M. and Gray, J.E.
TITLE	Isolation of two cDNA clones for phosphoinositide-specific phospholipase C from epidermal peels (accession no. X95877) and guard cells (accession no. Y11931) of Nicotiana rustica (PGR97-086) Plant Physiol. 114, 748-748 (1997)
JOURNAL	2 (bases 1 to 2013)
REFERENCE	Pical, C.
AUTHORS	Direct Submission
TITLE	Submitted (19-MAR-1997) C. Pical, University of Sheffield,
JOURNAL	Molecular Biology and Biotechnology, Western Bank, PO Box 594, Sheffield, S10 1QS, UK
FEATURES	Location/Qualifiers
source	1..2013
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	/product="1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase"
	/protein_id="CAA72681.1"
	/db_xref="GI:2765140"
	/db_xref="SPRMBL:O49902"
	/translation="MGSYVCVCFTRKFRVTEAEPPSDVKEAFKFKYANGNOMNSBOL LKFLIEVOGETLFTVGDSDVIVRILQKRPITKLTROTLEALDFHFLVFNLTOLNPII NVKHHMDNAPLSHYFIFLTHGNSYLQNLGTSQSDVPIIKALKKGVLELDIWNPS DKDDIHLVHGRTYFIVPELLEKLSIKHEAFVSPVPIVITLEDHLPDLOAKYAML TETCEMLFVPESDLEKCEPPELAKHRLIVSTKPKPKYLEASSTVSKERRNSOR SNEDEDDVMGTPELSLADQBEENEKSDSDFEDDCNHRPQFASAYKLTIAHGRP KGLLEALKVDPDKVRRLISLSEALEKMAESHGTEIVRFTORNLRVLPKLVGNPNEVED YLPLTGMHGAQMVAFNMQGYGRALMLHMGFRSNGCGYVVKVPDFLNLVGNPNEVED PRKALPVKTLKLVKVMGDGWHLDKOTHFEDLYSPDPFVTRVGIAGVPADEIMTKTKT KEDKTPVWDEAFTEPLTVPELALLRIEVEHYDMSEKDDFAGOTCIPISLKPGLIHAV PLCDRKGKISVSVLLMRFEV"
CDS	647 a 357 c 435 g 574 t
BASE COUNT	
ORIGIN	
Query Match	10.5%; Score 224.6; DB 8; Length 2013;
Best Local Similarity	49.9%; Pred. No. 6.6e-57;
Matches	871; Conservative
QY	222 atgagtcgaggggtgtgctgaattcttcacacagagcaaggggagtcgactccac 281
Db	155 ATGAATTCAGAACAGTACTGAAATCTTGATTCAGTACAGAGAGAGACCCCTTTTCACT 214
QY	282 ctgatgacgcacagcagatcatggagcgattctcgaaggagctggaagaatccttcgga 341
QY	215 GTTGCGTATTCATGTCATCTGTCATCTGTCGCAATCC-----TTCAGAAAGACACCCCATTA 269
Db	342 ctgcctctatcaactcagactgtctgaaggaggcttttcggaagtactgtatgaatccc 401
QY	270 CTAAGTTAACTCGTCAAACTCTTG-CTCTTGAAGATTTTCATCATTTTCTCTTCATACC 328
Db	402 gactgaatggcgtcttcacacacgttgttcacacacatgacgacgacgacgacgac 461
QY	329 GACCTTAATCCCAATTAATTAAGTTTACCATGATGATGATGATGATGATGATGATGAT 388
Db	462 tatttcattacagggccataactcgtacactgaccggaacacagctgagcagcagcagc 521
QY	389 TATTTTATATATCCCGGCATATCTTACTTGTGCTGGGAATCAATTGACGAGTATTGC 448
Db	522 agcagacacacccatcgtcgcgacactcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 581
QY	449 AGTGATGTCCTCAATTAATTAAGGCACTGAAAGAGGCTGAAGAGTATAGAGCTTGATATA 508

RESULT 15
NRY11931
LOCUS N.rustica mRNA for 1-phosphatidylinositol-4,5-bisphosphate
DEFINITION
phosphodiesterase.
Y11931
ACCESSION Y11931.1
VERSION Y11931.1
KEYWORDS 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase.
SOURCE Aztec tobacco.

us-09-828-447-7.rge

Sun Jul 28 10:34:38 2002

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 26, 2002, 17:22:17 ; Search time 63.5 seconds
(without alignments)
1710.879 Million cell updates/sec

Title: US-09-828-447-12
Perfect score: 3328
Sequence: 1 MCSIACCRSGTPKGPEDL.....MLFHFKCKCTQDFTAPISS 628

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues 562222

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: sp-archaea.*	2: sp-bacteria.*	3: sp-fungi.*	4: sp-human.*	5: sp-invertebrate.*	6: sp-mammal.*	7: sp-mhc.*	8: sp-organelle.*	9: sp-phage.*	10: sp-plant.*	11: sp-rodent.*	12: sp-virus.*	13: sp-vertebrate.*	14: sp-unclassified.*	15: sp-rvirus.*	16: sp-bacteriap.*	17: sp-archaeap.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1338	40.2	553	10 Q43442	Q43442 glycine max
2	1293	38.9	549	10 P93620	P93620 vigna ungui
3	1259.5	37.8	588	10 O49902	O49902 nicotiana r
4	1253.5	37.7	588	10 P93341	P93341 nicotiana r
5	1251.5	37.6	600	10 Q43443	Q43443 glycine max
6	1249	37.5	593	10 Q93YX8	Q93YX8 medicago tr
7	1241.5	37.3	600	10 Q43439	Q43439 glycine max
8	1234	37.1	551	10 Q43444	Q43444 glycine max
9	1225.5	36.8	585	10 O49952	O49952 solanum tub
10	1225	36.8	591	10 Q940R9	Q940R9 arabidopsis
11	1225	36.8	597	10 Q940Y9	Q940Y9 arabidopsis
12	1219.5	36.6	594	10 O24297	O24297 pisum sativ
13	1202.5	36.1	581	10 Q9XEK4	Q9XEK4 brassica na
14	1194	35.9	605	10 Q9M5Q2	Q9M5Q2 nicotiana t
15	1192.5	35.8	565	10 O49951	O49951 solanum tub
16	1175	35.3	596	10 O49950	O49950 solanum tub

17	1171.5	35.2	581	10 Q39033	Q39033 arabidopsis
18	1165	35.0	586	10 Q9M5Q5	Q9M5Q5 nicotiana t
19	1164	35.0	909	10 Q9LUZ0	Q9LUZ0 arabidopsis
20	1157	34.8	630	10 Q9FSW1	Q9FSW1 digitaria s
21	1155	34.7	584	10 Q9LY51	Q9LY51 arabidopsis
22	1132.5	34.0	599	10 Q9AXF1	Q9AXF1 oryza sativ
23	1104	33.2	561	10 Q39032	Q39032 arabidopsis
24	1100	33.1	561	10 O49970	O49970 arabidopsis
25	1030.5	31.0	526	10 Q9SZN3	Q9SZN3 arabidopsis
26	994.5	29.9	533	10 Q38811	Q38811 arabidopsis
27	748	22.5	531	10 Q9STZ3	Q9STZ3 arabidopsis
28	747	22.4	531	10 Q42582	Q42582 arabidopsis
29	698.5	21.0	613	4 Q96FL6	Q96FL6 homo sapien
30	695	20.9	762	4 Q9BRC7	Q9BRC7 homo sapien
31	680.5	20.4	513	10 Q9SD51	Q9SD51 arabidopsis
32	659.5	19.8	772	11 Q62711	Q62711 rattus norv
33	656.5	19.7	502	13 Q91423	Q91423 catfish, ph
34	650.5	19.5	787	4 Q9UPT3	Q9UPT3 homo sapien
35	636	19.1	771	11 Q63693	Q63693 rattus norv
36	629.5	18.9	640	6 Q95JS0	Q95JS0 macaca fasc
37	628	18.9	641	6 Q95JS1	Q95JS1 macaca fasc
38	623.5	18.7	751	5 Q21754	Q21754 caenorhabdi
39	603.5	18.1	745	11 Q60450	Q60450 cricetus
40	601.5	18.1	756	11 Q921B4	Q921B4 mus musculu
41	599.5	18.0	738	5 Q97037	Q97037 hydra magni
42	586.5	17.6	1154	4 Q9UPR0	Q9UPR0 homo sapien
43	581.5	17.5	1128	11 Q9QXG1	Q9QXG1 mus musculu
44	570	17.1	725	5 Q96101	Q96101 trypanosoma
45	570	17.1	725	5 Q9TZN8	Q9TZN8 trypanosoma

ALIGNMENTS

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Q43442	PRELIMINARY;	PRT;	553 AA.
ID Q43442			
AC Q43442;			
DT 01-NOV-1996 (TEMBLrel. 01, Created)			
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)			
DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)			
DE PHOSPHINOSITIDE-SPECIFIC PHOSPHOLIPASE C P12.			
OS Glycine max (Soybean).			
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;			
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.			
OX NCBI_TaxID=3847;			
EN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN-CV. WILLIAMS 82; TISSUE-ETIOLATED HYPOCOTYLS;			
RA Clouse J.A.;			
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.			
DR EMBL; U41473; AAB03257.1; -.			
DR HSSP; P10688; 1DJH.			
DR InterPro; IPR000008; C2.			
DR InterPro; IPR001192; PI-PLC.			
DR InterPro; IPR000909; PI-PLC_X.			
DR InterPro; IPR001711; PI-PLC_Y.			
DR Pfam; PF00168; C2; 1.			
DR Pfam; PF00388; PI-PLC-X; 1.			
DR Pfam; PF00387; PI-PLC-Y; 1.			
DR PRINTS; PR00390; PHPLIPASEC.			
DR ProDom; PD001202; PI-PLC_Y; 1.			
DR SMART; SM00239; C2; 1.			
DR SMART; SM00148; PLCXC; 1.			
DR SMART; SM00149; PLCYC; 1.			

RESULT 3
49902
D O49902
PRELIMINARY;
PRT; 588 AA.

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us-09-828-447-12.rspt

Sun Jul 28 10:34:37 2002

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AC 049902;
DT 01-JUN-1998 (TREMELrel. 06, Created)
DT 01-JUN-1998 (TREMELrel. 06, Last sequence update)
DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)
DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)
DE 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE (EC
DE 3.1.4.11).
DE Nicotiana rustica (Asteraceae).
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4093;
RN [1]
RP SEQUENCE FROM N.A.
RA Pical C., Kopka J., Muller-Rober B., Hetherington A.M., Gray J.E.;
RT "Isolation of two cDNA clones for phosphoinositide-specific
RT phospholipase C from epidermal peels (accession no. X95877) and guard
RT cells (accession no. Y11931) of Nicotiana rustica (PGR97-086).";
RL Plant Physiol. 114:748-748(1997).
DR EMBL; Y11931; CAA72681.1; -.
DR HSSP; P10688; 1DJH.
DR InterPro; IPR000008; C2.
DR InterPro; IPR001192; PI_PLC.
DR InterPro; IPR009099; PI_PLC_X.
DR InterPro; IPR001711; PI_PLC_Y.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00388; PI-PLC-X; 1.
DR Pfam; PF00387; PI-PLC-Y; 1.
DR PRINTS; PR00390; PHPLIPASEC.
DR PRODOM; PD001202; PI_PLC_Y; 1.
DR SMART; SM00239; C2; 1.
DR SMART; SM00148; PLCXC; 1.
DR SMART; SM00149; PLCYC; 1.
DR PROSITE; PS50004; C2_DOMAIN_2; 1.
DR PROSITE; PS50007; PIPLC_X_DOMAIN; 1.
DR PROSITE; PS50008; PIPLC_Y_DOMAIN; 1.
DR Hydrolase. 588 AA; 66942 MW; C132712EE2E1220E CRC64;
SQ SEQUENCE 588 AA; 66942 MW; C132712EE2E1220E CRC64;

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DB 18 EAEPPSD-VKEAFKKAENGOMNSEQLLKFLIEVQGETLFTVGDSVFI---VRQLQKR 73
QY 72 FGLASI-NSDLSKEAFKRYLNPDLNGVLHVHVDMPQMSHYFTFTGHNSYLTGNQLS 130
DB 74 HPITKLTROTALAEHFHFLFNTDLPNPINKVHDMNAPLSHYFTFTGHNSYLTGNLT 133
QY 131 SDSSTPTIAAALRGVRVVELDLWPD-DKGMKVTHGNTLTNPVSFOKCVTAIKNAFFT 189
DB 134 SDSDVPIKALKKGVRIELDWPNKDDIHVLHGRTVTPVELIRCLSKIKEHAFVA 193
QY 428 NYGAQVAVNMQGYGRALWLMHGMFRSNGCGYKVPDFLLNVPNNNEVDFPKAKLPVK 459

Query Match 37.7%; Score 1253.5; DB 10; Length 588;
Best Local Similarity 44.0%; Pred. No. 8.6e-79;
Matches 267; Conservative 94; Mismatches 203; Indels 43; Gaps 13;

QY 13 KGDPQDLVGEVFTIYSEN-ERMSAEGLLKFLHTEQGVDFTLDDAKQIMERIRKDWKS 71
DB 18 EAEPPSD-VKEAFKKAENGOMNSEQLLKFLIEVQGETLFTVGDSVFI---VRQLQKR 73
QY 72 FGLASI-NSDLSKEAFKRYLNPDLNGVLHVHVDMPQMSHYFTFTGHNSYLTGNQLS 130
DB 74 HPITKLTROTALAEHFHFLFNTDLPNPINKVHDMNAPLSHYFTFTGHNSYLTGNLT 133
QY 131 SDSSTPTIAAALRGVRVVELDLWPD-DKGMKVTHGNTLTNPVSFOKCVTAIKNAFFT 189
DB 134 SDSDVPIKALKKGVRIELDWPNKDDIHVLHGRTVTPVELIRCLSKIKEHAFVA 193
QY 190 SEYPCVCTIEDHLSLSEQALEKAAESHGTEIVRTQRIILRVYPKGTRENSNYPKPLGW 399
QY 428 NYGAQVAVNMQGYGRALWLMHGMFRSNGCGYKVPDFLLNVPNNNEVDFPKAKLPVK 459

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DR PS5008; PIPLC_Y_DOMAIN; 1..
SQ SEQUENCE 600 AA; 68696 MW; EC1778F1BB3B27ED CRC64;

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Query Match          37.6%; Score 1251.5; DB 10; Length 600;
Best Local Similarity 45.8%; Pred. No. 1.2e-78;
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Db 31 LFNEXSELMTPSHLKRFVLDVQRQEKATVEDQAIIIDFSRHFHRRGAG-----LNL 83
QY 84 EAFRYLAMPDLNGVL-HNVVHODMTPMSHXYEFTGHNSYLTGNQLSDSDSDTPIAAAL 142
Db 84 EFTFYFLSDDNPPLLPSHGVDHMTPLSHVFTVYGHNSYLTGNQLSDSDSDVPIINAL 143
QY 143 RGRVRVVELDWPD-DKGGMKVTHGNTLNPVYSFOKCVATKNNAFFTSEVPCVTIEDH 201
Db 144 KGVVRVIELDWPNASKDSIDLVLGRTLTPTVELIRCLRSIKDHAFVASEVPVITLEDH 203
QY 202 LTSLEQHAHAIEILQILGALYPPPTDALVEFPSPESLKRKRIIISTKPKKEYLEACSTQ 261
Db 204 LTPDLQAKVAEMTQFGDIL-FTPNSEVKEFTSPESLKRKRIIISTKPKKEYLEAKEKE 262
QY 262 KLAMENNLVEELEKEDKLEQTTTFAPLEENHILGENTPSPSRKEVEVLSOKENSTPAELNS 321
Db 263 K-----GDSSQHEKGGDSEHGKAS--GEDAWGKEVPSL-KGGTIEDYKDNVDEDLND 315
QY 322 RSPSDILEGATSTRYSKSDNGDNPKNFKFYARLITRLAKHAKGTSMEHRLQVD-ESVKRI 380
Db 316 EEEFD-----ESDKSHHNEAP---EYRHLLAIHAGK-PRGGLVE-CLKYDPEKVRRL 362
QY 381 SLSESKLEKRVKEWPEALVKFTQKNILRVVYPAANRVVNSNFCPTLAWNYQAWMAQNMQG 440
Db 363 SLSEQOLEKAAIYNGQQIVRTQTNILRVYPKGTRIDSSNYPNPLIGWHMGAQWAFVFNMQG 422
QY 441 YGKELWQAFKFGKNGCGGYLVKPOYLENLLPSGVFPNFTSPRNTTLILKLVMTTIGWD 500
Db 423 YGRSLWLMHGFWRANGCGGVKKPNPFLLETGDPDEVFNPKAKLPVTKTLKVTVYWGSGWY 482
QY 501 KAFSKRHFDLSPDPFTRVIVVGVGPADEAKWKTSVSDNSWAPHNWDEHFEALCKPELAL 560
Db 493 YDFKHTHFDQSPDFYTRVIGIAGVNDTIMKRTKAIEDNLPTWNEAFEPFTVTPPELAL 542
QY 561 LRIEVRDHHDDSDKDEFEGOTCLPIHEVRDGYECMQMDKKGNVLKGLVLMFLHFQ 614
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RESULT	6		
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DT	01-DEC-2001	(TReMBLrel. 19, Last sequence update)	
DT	01-DEC-2001	(TReMBLrel. 19, Last annotation update)	
DE	PHOSPHONOSITIDE-SPECIFIC	PHOSPHOLIPASE C.	
GN	PLC1.		
OS	Medicago truncatula	(Barrel medic).	
OC	Eukaryota;	Viridiplantae;	Streptophyta;
OC	Spermatophyta;	Magnoliophyta;	Embryophyta;
OC	eudotsids I;	Fabales;	Fabaceae;
OX	NCBI_TaxID=3880;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RT	Engstrom E.M., Long S.R.;		
RT	"MPLCL1, a putative phospholipase C from		
RT	Medicago truncatula."		
RT	Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AY059631; AAL17948.1;		
ISQ	SEQUENCE	593 AA; 67419 MW; AA37967169DAE4A5	CRG64;

glucose T A :
 ... /conPank /MDBJ databases.

Clouse J.A.;
Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.

Query Match 37.5%; Score 1249; 17;
Best Local Similarity 45.5%; Pred. No. 1.8e-78;
Matches 282; Conservative Indels 54; Gaps
Matches 85; Mismatches 199;

[illegible]

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RESULT      7
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DT          01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DD          01-NOV-1996 (TREMBLrel. 19, Last annotation update)
DT          01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE          PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE C.
OS          Glycine max (Soybean); Streptophyta; Tracheophyta;
DS          Eukaryota; Viridiplantae; eudicotyledons; core eudicots; Rosidae;
OC          Spermatophytes; Magnoliophyta; euclcotyledons; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
CC          eurosids I; Fabales; Fabaceae;
CX          NCBI_TaxID=3847;
RN          [1]
RP          SEQUENCE FROM N.A.
RC          STRAIN-CV. WILLIAMS 82; TISSUE-ETIOLATED HYPOCOTYLS;
RX          MEDLINE=96045546; PubMed=7550376;
RA          Shi J., Gonzales R.A., Bhattacharya M.K.;
RT          "Characterization of a plasma membrane-associated phosphoinositide-specific phospholipase C from soybean.";
RL          Plant J. 8:381-390(1995).
RN          [2]
RP          SEQUENCE FROM N.A.
RC          STRAIN-CV. WILLIAMS 82; TISSUE-ETIOLATED HYPOCOTYLS;
RX          [2]

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clause J.A.:

Clouse J.A.;
Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.

Query Match 37.5%; Score 1249; 17;
Best Local Similarity 45.5%; Pred. No. 1.8e-78;
Matches 282; Conservative Indels 54; Gaps
Matches 85; Mismatches 199;

[illegible]

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RESULT      7
Q43439     PRELIMINARY;          PRT:    600 RA.
ID
Q43439;
AC Q43439; 1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TREMBLrel. 19, Last annotation update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE C.
DS Glycine max (Soybean);
OS Streptophyta; Embryophyta; Tracheophyta;
OC Eukaryota; Viridiplantae; eudicotyledons; core eudicots; Rosidae;
OC Spermatophytes; Magnoliophyta; euclerodiales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OC eurosids I; Fabales; Fabaceae;
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. WILLIAMS 82; TISSUE-ETIOLATED HYPOCOTYLS;
RX MEDLINE=96045546; PubMed=7550376;
RA Shi J., Gonzales R.A., Bhattacharya M.K.;
RT "Characterization of a plasma membrane-associated phosphoinositide-specific phospholipase C from soybean.";
RL Plant J. 8:381-390(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. WILLIAMS 82; TISSUE-ETIOLATED HYPOCOTYLS;
RX

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clause J.A.:

Clouse J.A.;
Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.

Query Match 37.5%; Score 1249; 17;
Best Local Similarity 45.5%; Pred. No. 1.8e-78;
Matches 282; Conservative Indels 54; Gaps
Matches 85; Mismatches 199;

[illegible]

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RESULT      7
Q43439     PRELIMINARY;          PRT:    600 RA.
ID
Q43439;
AC Q43439; 1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TREMBLrel. 19, Last annotation update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE C.
DS Glycine max (Soybean);
OS Streptophyta; Embryophyta; Tracheophyta;
OC Eukaryota; Viridiplantae; eudicotyledons; core eudicots; Rosidae;
OC Spermatophytes; Magnoliophyta; euclerodales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OC eurosids I; Fabales; Fabaceae;
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. WILLIAMS 82; TISSUE-ETIOLATED HYPOCOTYLS;
RX MEDLINE=96045546; PubMed=7550376;
RA Shi J., Gonzales R.A., Bhattacharya M.K.;
RT "Characterization of a plasma membrane-associated phosphoinositide-specific phospholipase C from soybean.";
RL Plant J. 8:381-390(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. WILLIAMS 82; TISSUE-ETIOLATED HYPOCOTYLS;
RX

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01-DEC-2001 (TRENBLREL 19, Last annotation update)
PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C P25.
Glycine max (Soybean).
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
eucotyledons; core eudicots; Rosidae;
Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
NCBI_TaxID=3847;
SEQUENCE FROM N.A.
STRAIN=CV. WILLIAMS 82; TISSUE=ETIOLATED HYPOCOTYLS;
Shi J., Gonzales R.A., Bhattacharya M.K.;
Phosphoinositide-specific phospholipase Cs contain a C-terminal
domain having homology to the C2 domain of protein kinase C.;
Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
[2]
SEQUENCE FROM N.A.
STRAIN=CV. WILLIAMS 82; TISSUE=ETIOLATED HYPOCOTYLS;
Clouse J.A.;
Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
EMBL: U01475; AA03259.1;
HSP; P10688; IDJH.
InterPro: IPR000008; C2
InterPro: IPR001192; PL-PLC.
InterPro: IPR000909; PL-PLC-X.
Pfam: PF001711; PL-PLC-Y.
Pfam: PF00168; C2; 1.
Pfam: PF00388; PL-PLC-X; 1.
Pfam: PF00387; PL-PLC-Y; 1.
PRINTS: P000390; PHPLIPASEC.
ProDom: P0001202; PL-PLC_Y; 1.
SMART: SM00239; C2; 1.
SMART: SM00148; PLCXC; 1.
SMART: SM00149; PLCYC; 1.
PROSITE: PS50004; C2.DOMAIN.2; 1.
PROSITE: PS50007; PL-PLC-X.DOMAIN; 1.
PROSITE: PS50008; PL-PLC-Y.DOMAIN; 1.
SEQUENCE 551 AA; 62472 MW; CEC777A2FC151C7D CRC64;

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QY 253 EYLEACSTOKLAMENRNLVEELEKEDKLEQTTAPLEENHILGENTPSPSRKEVEVLSOKE 312
|||:|
Db 256 EYLOA-----KEVNETGAMKGT-----OTDEANGREV 284
|||:|
QY 313 MSTPAELNSPSDLGRA-TSTRYSKSNDGNDPNKPKFYARLITIRLAKHAKGTSMEHRL 371
|||:|
Db 285 SDIKARYNDRDSDDEGEADSDDEEDPTSQONTAP---EYRLIAIHAGKGGGLS--DWL 339
|||:|
QY 372 QVD-ESVKRLISLESLEKVEKPEALVKFTOKNLRVYPAANRVNSNFCPTLAWNTG 430
|||:|
Db 340 RVPDVKVRRRLSLEQELGKAVVTHGEIIRFTQRTNLRIRYPKGIRDSNPNFNAWTHG 399
|||:|
QY 431 AQVAAQNMCGYGRLEWQAFKFGKGGCGYVLPQVLLNLPSPGFNPPTS--PRNTTLI 488
|||:|
Db 400 AQVAFNMCGYGRSLMLHMGFGNGCGYVKKPDILLKAGPNNEVDFDEANLPVKIT-- 457
|||:|
QY 489 LKTKVMTLGDWAKAFKRHFDLSPDPFFTRVIVGVPADEAKWKTSVVDNSWAPHNED 548
|||:|
Db 458 LKTVFMGEGWYDFEHTHFDAYSPPDFYARIGIAGVDADIVMKTKTTLEDNWIPTWDEQ 517
|||:|
QY 549 HEFALCPALALRIEVRDHDSDSKDEFEGQCTLPHEVRDGYRCMQMDKGNVLKGYL 608
|||:|
Db 518 FEFLTVPELALLURVEHYEDMSEKDDFAGQCTCLPSELROGIRAVPLHNRKGEKYNVK 577
|||:|
QY 609 MLFHFQ 614
|||:|
Db 578 LLRLFE 583
|||:|

RESULT 10
Q940R9 PRELIMINARY; PRT; 591 AA.
ID Q940R9;
AC Q940R9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PHOSPHINOSITIDE-SPECIFIC PHOSPHOLIPASE C4.
GN PLC4.
OS Arabidopsis thaliana (Mouse-ear cross).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Pical C.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY053422; AAL23439.1; -.
SQ SEQUENCE 591 AA; 67335 MW; 67CC1169F422BE22 CRC64;

Query Match 36.8%; Score 1225; DB 10; Length 591;
Best Local Similarity 43.4%; Pred. No. 8.3e-77;
Matches 269; Conservative 101; Mismatches 206; Indels 44; Gaps 13;

QY 2 CSIACRSTPKDPEQDILVGEVFTIYSENE-RMSAEGLLKFLHTEQGDVDFTLDDAKQI 60
|||:|
Db 7 CLIFTRKFRMTESGPVED-VRLDFEKYTEGDAHMSPEQLQKLWTEEGEGETSLEAERI 65
|||:|
QY 61 MERIRKDWKSGSLASINSLSKAERKLYMNPDLNGLVHNVHODMTQPHSHYFIPTGH 120
|||:|
Db 66 DEVILR--RKHHIAKTRNLDFDNFYLFSTDLNPIADQVHQNMDAPLSHYFIPTGH 123
|||:|
QY 121 NSYLTGNLSSDSDTPIAAALRRGVVVVLDLPDPPDKGGMKVTHGNTLTNPVSFOKCVT 180
|||:|
Db 124 NSYLTGNLSSNCSELPADALRRGVVVVLDLPDPPDKGGMKVTHGNTLTNPVSFOKCVT 183
|||:|
QY 181 AKNNAFTTSEYPCVCTIEDHILTSLOQHAFILEQILGDALYYPPTTDLVFPSPSL 240
|||:|
Db 184 SIKANAFALSKYPVITLEDHLTPKLOPKVAKMITQTEGDMLYY-HDSQGCQEPSPPEL 242
|||:|
QY 241 KRKLIISTKPPREYLEACSTOKLAMENRNLVEELEKEDKLEQTTAPLEENHILGENTPS 300
|||:|

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Db 243 KKKILISTKPPREYLEA-----NDTKEKDNKGKDS-----DEDVWG----- 280
|||:|
QY 301 LRKEVEVLSQKEMSTPAELN--SRSPDLGEATSTRYSKSNDGNDPNKPKFYARLITIRL 358
|||:|
Db 281 --KEPEDL-----ISTQSDLDKVTSSVNDLNQDDEERGSCESDTSQOLQAPVKRLIAHA 334
|||:|
QY 359 AKHAGTSMHERLQVD-ESVKRLISLESLEKVEKPEALVKFTOKNLRVYPAANRVN 417
|||:|
Db 335 GKPKGGLRM--ALKVDPNKRIRLSLEQLEKAVASYGADVIREFTQKNFLRIYPKGTRFN 392
|||:|
QY 418 SENFCTPLAWNYGAQWVAQNMCGYGRLEWQAFKFGKGGCGYVLPQVLLNLPSPGVPF 477
|||:|
Db 393 SSNYAPQICWWSGAQMIAFNMCGYGRALWLMGEMFRANGCGYVKKPDLMDASPNGQDF 452
|||:|
QY 478 NP---TSPRNTTLILIKIVMTTLGWDKAFKRHFDLSPDPFFTRVIVGVPADEAKWKT 534
|||:|
Db 453 YPKDNSSPKKT---LKVKVMCGDGLLDFKKTHTFDSDYSPDPFFVVRVGTAGAPVDEWKT 509
|||:|
QY 535 SVVDNSWAPHNEDHEFALKCPPELALLRIEVRDHDSDSKDEFEGQCTLPHEVRDGYRCM 594
|||:|
Db 510 KLEYDTWTPIWNKEFTFPLAVPELALLRVEHEDVNEKDDFGGQCTCLPVSSEIRQIRAV 569
|||:|
QY 595 QMYDKKGNVLKGYLMLFHFQ 614
|||:|
Db 570 PLFNEKGVKYSSTRLLMRFE 589
|||:|

RESULT 11
Q9LUY9 PRELIMINARY; PRT; 597 AA.
ID Q9LUY9;
AC Q9LUY9;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PHOSPHINOSITIDE-SPECIFIC PHOSPHOLIPASE C.
OS Arabidopsis thaliana (Mouse-ear cross).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=COLUMBIA;
RC MEDLINE=20181125; PubMed=10718197;
RX Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence
RT features of the regions of 3,076,755 bp covered by sixty P1 and TAC
RT clones."
RL DNA Res. 7:31-63(2000).
DR EMBL; AB020755; BAA97338.1; -.
DR HSP; P10688; IDJH.
DR InterPro; IPR000008; C2.
DR InterPro; IPR001192; PI_PLC.
DR InterPro; IPR000909; PI_PLC_X.
DR InterPro; IPR001711; PI_PLC_Y.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00388; PI-PLC-X; 1.
DR Pfam; PF00387; PI-PLC-Y; 1.
DR PRINTS; PR00390; PHPLIPASEC.
DR ProDom; PD001202; PI_PLC_Y; 1.
DR SMART; SM00239; C2; 1.
DR SMART; SM00148; PLCXC; 1.
DR SMART; SM00149; PLCYC; 1.
DR PROSITE; PS50004; C2_DOMAIN_2; 1.
DR PROSITE; PS50007; PIPLC_X_DOMAIN; 1.
DR PROSITE; PS50008; PIPLC_Y_DOMAIN; 1.
SQ SEQUENCE 597 AA; 68038 MW; 176D1715653AF82B CRC64;

Query Match 36.8%; Score 1225; DB 10; Length 597;
Best Local Similarity 43.4%; Pred. No. 8.4e-77;

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Matches 269; Conservative 101; Mismatches 206; Indels 44; Gaps 13;

QY 2 C2ACACRGTGKDPDQVLGVFTIYSENE-RMSAEGLLKFLHTEQGVDFTLDDAKOI 60
 Db 13 CLIFTRKFRMTESGPVED-VRLFEXYTGSDAHMSPEQLOKLWTEGEGEETSLSEAEERI 71
 QY 61 MERIKDKWKSFGSLASINDLSKEAFKRYKLYMNPDLGVHNVHODMTQPMSHYFIYFTGH 120
 Db 72 VDEVLK--RKHHIAKFTRRNLTLDDNYFLFSTDLNPPIADOVHQNMDAPLSHYFIYFTGH 129
 QY 121 NSYLTGNSLSSDSDPIAALRRGVVRVVELDLWPDKGMKVTHGNTLTNPVSFKCVT 180
 Db 130 NSYLTGNSLSSSELPIDALRRGVVRVVELDLWPDGTDVCKGRTLTKEVKGKCLE 189
 QY 181 AKNNAFFFTSEYPCVTIEDHTSETLQGHAAEILEQILDALYPTPTDALTVEFFSPESL 240
 Db 190 SIKANAFALSKYPIVITLEDHLPKLOFKVAKMITQTFGDMLYY-HDSGQCQEFFSPEEL 248
 QY 241 KRILISTPPKYLEACSTQKLAENRNVLVELEKEDKLEQTFAPLEENHILGENTPS 300
 Db 249 KEKILISTPPKYLEA-----NDTKKONGEKGKDS-----DEDVWG----- 286
 QY 301 LRKEVEVLQKSTPAELN--SRSPDLGEATSTRYSKSNDGNDNPKHKFYARLTITRL 358
 Db 287 --KEPEDL----ISTOSDLDKVTSSVNDLNQDDEERGSCESDTSCOLQAPAYKALIAHA 340
 QY 359 AKHAKGTSMEHRLQVD-ESVKRISLSSEKLEKVVKEWPEALVKFTQKNILRVYPAANRYN 417
 Db 341 GKPKGGLRW--ALKVDPNKIRLSLSEQLLEKAVASGADVIRFTQKNFLRIYPKGTREN 398
 QY 418 SSNFCPTLAWNYGAQVAQNMGGYKELWQAFKFGNGCGGVYKLPQVYLENLPSGVFP 477
 Db 399 SSNYKQKQIGMGAQMAFANMGGYGRALWLMGEMFRANGCGYVKKPDPFMDASPNQDF 458
 QY 478 NP--TSRPTNTLLIKVMTTLTGWDKAFSKRHFDFLSPDPFTRVIVGVVPADEAKWKT 534
 Db 459 YPKDNSPKPT---LKKVCMGQGLWLLDFKTHFDSYSPDPFVRVGIAGAPVDEVWEKT 515
 QY 535 SVYDNSWAPHNEDHEFALKCPALALLRIEVRDHDHDDSKDEFEGQTCPLPIHEVRDGYROM 594
 Db 516 KIEYDTWPIWNKEFTPLAVPEALLRVEVHEHDVNEKDDFGGQTCPLVPSEIROGIRAV 575
 QY 595 QMTDKKGNVLKGVLMFLHFQ 614
 Db 576 PLFNRRGVKYSTRLMRFE 595

RESULT 12
 O24297
 ID O24297 PRELIMINARY; PRT; 594 AA.
 AC O24297;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE PHOSPHOLIPASE C.
 GN PLC.
 OS Pisum sativum (Garden pea).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
 OX NCBI_TaxID:3888;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LEAF;
 RA Venkataraman G., Reddy M.K., Sopory S.K.;
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Y15253; CAA75546.1; --
 DR HSSP; P10688; 1DJH.
 DR InterPro; IPR000008; C2.
 DR InterPro; IPR001192; PI_PLIC.
 DR InterPro; IPR000909; PI_PLIC_X.
 DR InterPro; IPR001711; PI_PLIC_Y.
 DR Pfam; PF00168; C2; 1.

DR Pfam; PF00388; PI-PLIC-X; 1.
 DR Pfam; PF00387; PI-PLIC-Y; 1.
 DR PRINTS; PR00390; PHPLIPASEC.
 DR ProDom; PD001202; PI_PLIC_Y; 1.
 DR SMART; SM00239; C2; 1.
 DR SMART; SM00148; PLCXC; 1.
 DR SMART; SM00149; PLCYC; 1.
 DR PROSITE; PS50004; C2_DOMAIN_2; 1.
 DR PROSITE; PS50007; PIPIC_X_DOMAIN; 1.
 DR PROSITE; PS50008; PIPIC_Y_DOMAIN; 1.
 SQ SEQUENCE 594 AA; 67446 MW; 8F4467B04AD33929 CRC64;

Query Match 36.68; Score 1219.5; DB 10; Length 594;
 Best Local Similarity 44.98; Pred. No. 2e-76;
 Matches 272; Conservative 100; Mismatches 187; Indels 47; Gaps 17;

QY 16 PEODLVGVFTIYS-ENERMSAEGLLKFLHTEQGVDFTLDDAKOIMERIKRDKWKSFG 74
 Db 27 PSQ--IRELYINYDESAIMTASHLQRLFLIEVQGDENITENEAGSII-----DGKHL 79
 QY 75 ASINDLSKEAFKRYKLYMNPDLGVHNVHODMTQPMSHYFIYFTGHNSYLTGNSLSSD 133
 Db 80 FH-RGLNLESEFLKFLFSDNKAPLLASGRVHVQVMSPLSHYIHTGHNSYLTGNSVSDC 138
 QY 134 SDTPIAALRRGVVRVVELDLWPD-DKGMKVTHGNTLTNPVSFKCVTAIKNNAFTSEY 192
 Db 139 SDAPITVALERGVRIEILDIPNGSKDDIEVLHGRTLTTPVALIKCLRSKEYAFVASEY 198
 QY 193 PVCVTIEDHLSLQGHAAEILEQILDALYPTPTDALTVEFFSPESLKRKIIISTPKPK 252
 Db 199 PVITLEDHLPDLOAKVAQVMTQTFGDLFC-PSSSELEKFEPSDLKRRIIISTPKPK 257
 QY 253 EYLEACSTQKLAENRNVLVELEKEDKLEQTFAPLEENHILGENTPSLR-KEVEVLSQK 311
 Db 258 EYLEA-----KEVQKEELTKGSSGDEE--AWGKEVSPSLRGGTISDYKNN 301
 QY 312 EMSPTAELNSRSPDLGEATSTRYSKSNDGNDNPKHKFYARLTITRLAKHAKGTSMEHRL 371
 Db 302 DDDDEDDLEEDSE--EAKSRONGSGE-----YRRLIAHAGK-PKGLVE-GL 348
 QY 372 QVD-ESVKRISLSSEKLEKVVKEWPEALVKFTQKNILRVYPAANRVSNNSFCPTLAWNYG 430
 Db 349 KVDPKVRRLSLSSEKLEKAAETGKEIVRTQKNILRVYPTQTRITSSNYPNLIQWGHG 408
 QY 431 AQMVAQNMGGYKELWQAFKFGNGCGGVYKLPQVYLENLPSGVPPNPFS--PRNTTLI 488
 Db 409 AQMVAQNMGGYGRSLWLMQGMFKANGCGGVYKLPDFLLKTGPNNEVDFPKASLPKTT-- 466
 QY 489 LKIKVMTTLGWDKAFSKRHFDFLSPDPFTRVIVGVVPADEAKWKTSDVNSWAPHNED 548
 Db 467 LKVTYMGEGWYDFDHTHFDQFSPDPFARVGIAGVFPDITMKTKTYVEDSWLPSWNEV 526
 QY 549 HEFALKCPALALLRIEVRDHDHDDSKDEFEGQTCPLPIHEVRDGYRCMQYDKKGNVLKGV 608
 Db 527 FEFPLSVFQALLRIEVEVHEVDMESEKDDFGGQTCPLPVWELRTGIRAVPLHSRKGDKYNNVK 586
 QY 609 MLFHFQ 614
 Db 587 LLMRPE 592

RESULT 13
 O24297
 ID O24297 PRELIMINARY; PRT; 581 AA.
 AC O24297;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE PHOSPHOLIPASE C.
 GN PLC.
 OS Brassica napus (Rape).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eudicots II; Brassicales; Brassicaceae; Brassica.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. WESTAR;
 RA Das S., Hussain A.K., Keller W.A., Georges F.:
 RT "Isolation and characterization of a full cDNA coding region for
 RT phosphoinositide-specific phospholipase C from *Brassica napus*, cv.
 RT Westar.";
 RL Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF108123; AAD26119.1; -;
 DR HSSP; P10688; IDJH.
 DR InterPro; IPR000008; C2.
 DR InterPro; IPR001192; PI-PLC.
 DR InterPro; IPR000909; PI-PLC_X.
 DR InterPro; IPR001711; PI-PLC_Y.
 DR Pfam; PF00168; C2; 1.
 DR Pfam; PF00388; PI-PLC-X; 1.
 DR Pfam; PF00387; PI-PLC-Y; 1.
 DR PRINTS; PR00390; PHPLIPASEC.
 DR PRODOM; PD001202; PI-PLC_Y; 1.
 DR SMART; SM00239; C2; 1.
 DR SMART; SM00148; PLCXC; 1.
 DR SMART; SM00149; PLCYC; 1.
 DR PROSITE; PS50004; C2_DOMAIN_2; 1.
 DR PROSITE; PS50007; PIPLC_X_DOMAIN; 1.
 DR PROSITE; PS50008; PIPLC_Y_DOMAIN; 1.
 SQ SEQUENCE 581 AA; 66274 MW; 3E98CF88F7EAD7DE CRC64;
 Query Match 36.1%; Score 1202.5; DB 10; Length 581;
 Best Local Similarity 44.4%; Pred. No. 2.9e-75;
 Matches 269; Conservative 90; Mismatches 174; Indels 73; Gaps 17;
 QY 21 VGEVFTIYSENERMSAEGLLKFLHTBOGDVFTLDDAKOIMERIRKDWKKSFGGLASI--N 78
 DB 27 VKTLEKYSNGWMTVDHLQRLVDVOKDKATKEDQSIIN-----AASSLLHS 76
 QY 79 SDSLKSAFRKYL---NPDLNGVLHVHVDTPMSPHYFTGHNSTLTGNSLSSDSS 135
 DB 77 NGLHDAFFKYLFGSDNNPL--ALHE-VHODMDAPISHVFTGHNSTLTGNSLSSDSC 133
 QY 136 TPIAAALRGVRVVELDLPD--DKGGMKVTGNTLTNPVSFOKCVTAIKNNAFTSEYPV 194
 DB 134 VPIIDALKGVRVIELDIWPNKNDIDVLHGRTLTSPVLIKCLRAIKTHAFVSDPY 193
 QY 195 CVTIEDHLTSELOGHAAEILEQILDALYYPPTTDALVEFPSPSLKRIIISTKPKKY 254
 DB 194 VTTLEDHLPLOSKVAEMVTEIFGEILFTPPVGESLKEFPSPSLKRIIISTKPKKY 253
 QY 255 LEACSTOKLAMENRNIVEELEKEDLEQTTAPLEENHILGENTPSLRKEVEVLSQKMS 314
 DB 254 KEG-----KDEVDVQKGKA-LGDEEVWGVREVPSE----- 281
 QY 315 TPAELN-SRSPSDLGEATSTRYSKNDGNDNPKHF-----YARLTIIRLAKHAKGTSM 367
 DB 282 --IERKSGDKDLDL-----EEDNDEDDVEFKKNAPQYKHLTAIHAGK--PKG-SI 331
 QY 368 EHRLOYD-ESVRIISLSSEKLEKVEKWPALVKFTQKNILRVYPAANRVNSSFCCPTLA 426
 DB 332 TACLAVDPDKVRRLSLESEOLEKAAEKYAKQIVRFTQNLRLIYPKTRVTSNNPLVG 391
 QY 427 WNYGQAMVAQNMGGYKGLQAFKFGKNGCGGVLPQYVLENLPSGVFPNP--TSRPN 484
 DB 392 WSHGQAMVAFNQYGRSLWLMQGMFRANGCGGYKPKPDLILGGSDSDIFDPKTLIPVK 451
 QY 485 TTLILKIKVMTLWGDKAFSKRRHFLFSPDFFTFRVTVWGVPADEAKWTSVVDNSWAPH 544
 DB 452 TT--LRVTIYMEGWYDFRTHFDQYSPDPFYTRVGIAGVPADYVMKTKTLEDNWFVS 509
 QY 545 WNEDEHFAKCPALALLRIEVRDHDHDSKDEFEGQTCCLPITHEVRDGRVCMQYDKKGNVL 604
 DB 545 WNEDEHFAKCPALALLRIEVRDHDHDSKDEFEGQTCCLPITHEVRDGRVCMQYDKKGNVL 604

Db 510 WDEVFEFPLTPEYALLRLLEVHEYDMSEKDDFGGTCCLPVWELQEGIRSFPLHNRKEKY 569
 QY 605 KGVLM 610
 DB 570 KSVKLL 575
 RESULT 14
 Q9M5Q2
 ID Q9M5Q2 PRELIMINARY; PRT; 605 AA.
 AC Q9M5Q2;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE PHOSPHOLIPASE C2.
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4097;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Goswami M., Singh B.N., Reddy M.K., Sopory S.K.;
 RL Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF223573; AAF33824.1; -;
 DR HSSP; P10688; IDJH.
 DR InterPro; IPR000008; C2.
 DR InterPro; IPR001192; PI-PLC.
 DR InterPro; IPR000909; PI-PLC_X.
 DR InterPro; IPR001711; PI-PLC_Y.
 DR Pfam; PF00168; C2; 1.
 DR Pfam; PF00388; PI-PLC-X; 1.
 DR Pfam; PF00387; PI-PLC-Y; 1.
 DR PRINTS; PR00390; PHPLIPASEC.
 DR PRODOM; PD001202; PI-PLC_Y; 1.
 DR SMART; SM00239; C2; 1.
 DR SMART; SM00148; PLCXC; 1.
 DR SMART; SM00149; PLCYC; 1.
 DR PROSITE; PS50004; C2_DOMAIN_2; 1.
 DR PROSITE; PS50007; PIPLC_X_DOMAIN; 1.
 DR PROSITE; PS50008; PIPLC_Y_DOMAIN; 1.
 SQ SEQUENCE 605 AA; 68634 MW; 1B8FAB26D1C64A50 CRC64;
 Query Match 35.9%; Score 1194; DB 10; Length 605;
 Best Local Similarity 43.0%; Pred. No. 1.2e-74;
 Matches 261; Conservative 101; Mismatches 183; Indels 62; Gaps 16;
 QY 21 VGEVFTIYSENERMSAEGLLKFLHTBOGDVFTLDDAKOIMERIRKDWKKSFGGLASIN-- 78
 DB 27 VKNLFNKYSNGVMAENLQRLIEVQKEENSIEDAGGINNLH-----DLKILNIF 79
 QY 79 --SDSLKSAFRKYL---NPDLNGVLHVHVDTPMSPHYFTGHNSTLTGNSLSSDSC 137
 DB 80 HRRGLHDAFFKYLFPADINPPINP--KRGIIHDMNEPLSHFYFTGHNSTLTGNSLSSDSC 137
 QY 134 SDTPIAAALRGVRVVELDLPD--DKGGMKVTGNTLTNPVSFOKCVTAIKNNAFTSEY 192
 DB 138 SDVPIIQAALRGVRVIELDIWPNKADDDVEVLHGTTLTTPVALIKCLRSIKHAFVSVEY 197
 QY 193 PCVTIEDHLTSELOGHAAEILEQILDALYYPPTTDALVEFPSPSLKRIIISTKPKK 252
 DB 198 PVVITLEDHLPLOKVAEMITQTFGDMFLSPDS--CLKNFSPSGSLKRRVLSTKPKK 255
 QY 253 EYLEACSTOKLAMENRNIVEELEKEDLEQTTAPLEENHILGENTPSLRKEVEVLSQKE 312
 DB 256 EYLOA-----KEVKEKDS--KKGTDAP-----DTEAMGREVSDLK--- 288
 QY 313 MSTPAELNRSRPSDLGEATSTRYSKNDGNDNPKHF-----KYARLTIIRLAKHAKGTSMEH 369
 DB 289 ---ARYNDKDDSDDGAGVED--DESDGDPNSQNVAPYKCLIAIHAGKGGGLS--D 340
 QY 370 LQYD-ESVRIISLSSEKLEKVEKWPALVKFTQKNILRVYPAANRVNSSFCCPTLAWN 428

```

Query Match          35.8%; Score 1192.5; DB 10; Length 565;
Best Local Similarity 42.7%; Pred. No. 1.4e-74;
Matches 259; Conservative 98; Mismatches 167; Indels 83; Gaps 14;

QY 21 VGEVFTIYSENER-MSAGLLKLFHTFEGQGVDETFDDAKQIMERIKRWKKFSFGLASINS 79
      : : |||: : ||| : : |||: : : : : |||: : :
Db 27 IKNLFRYSDDSGVMSVQNLHRLFIETQEKKNASLONAEAIINHHGDSKQ-----K 78

90 NYSKFAEPREVT---NMDPIKCVINNVVHODMTQPMSHYFTFTGHNSLYFTGNLSDSDST 136

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Search completed: July 26, 2002, 17:29:21
Job time: 424 sec

Search completed: July 26, 2002, 17:29:21
Job time: 424 sec

us-09-828-447-12.rag

Sun Jul 28 10:34:35 2002

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 26, 2002, 16:05:57 ; Search time 50.59 seconds
(without alignments)
1378.817 Million cell updates/sec

Title: us-09-828-447-12

Perfect score: 3328

Sequence: 1 MCSIACCRSGTGPQDGL.....MLFHQCKCTFQDTAPISS 628

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 11107396 residues 747574

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
- 2: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
- 3: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
- 4: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
- 5: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
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- 10: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
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- 14: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
- 15: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
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- 19: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
- 20: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1105	33.2	561	AA91932	Phosphatidylinositol-4,5-bisphosphate specific phospholipase C
2	698.5	21.0	736	AA91932	Human phospholipase C
3	698.5	21.0	789	AA91932	Human phospholipase C
4	695	20.9	787	AA91932	Human phospholipase C
5	650.5	19.5	736	AA91932	Human phospholipase C
6	594.5	17.9	736	AA91932	Human phospholipase C
7	559	16.8	1096	AA91932	Human phospholipase C
8	545.5	16.4	677	AA91932	Human phospholipase C
9	543	16.3	217	AA91932	Human phospholipase C
10	508.5	15.3	1809	AA91932	Human phospholipase C
11	501	15.1	1058	AA91932	Human phospholipase C

12	501	15.1	1216	22	AA91932	Human protein SEQ
13	474	14.2	1236	22	AA91932	Human protein SEQ
14	464.5	14.0	1312	22	AA91932	Human protein SEQ
15	430	12.9	178	21	AA91932	Human protein SEQ
16	428	12.9	869	15	AA91932	Human protein SEQ
17	418	12.6	567	22	AA91932	Human protein SEQ
18	414	12.4	173	21	AA91932	Human protein SEQ
19	409.5	12.3	1290	17	AA91932	Human protein SEQ
20	344	10.1	466	22	AA91932	Human protein SEQ
21	337.5	9.4	254	22	AA91932	Human protein SEQ
22	312	9.4	254	22	AA91932	Human protein SEQ
23	286.5	8.6	806	22	AA91932	Human protein SEQ
24	284.5	8.5	639	22	AA91932	Human protein SEQ
25	258	7.8	153	22	AA91932	Human protein SEQ
26	253	7.6	153	22	AA91932	Human protein SEQ
27	239	7.2	541	22	AA91932	Human protein SEQ
28	239	7.2	541	22	AA91932	Human protein SEQ
29	238	7.0	332	22	AA91932	Human protein SEQ
30	234.5	6.8	666	22	AA91932	Human protein SEQ
31	225	5.3	137	22	AA91932	Human protein SEQ
32	175.5	5.2	102	22	AA91932	Human protein SEQ
33	172.5	5.1	253	22	AA91932	Human protein SEQ
34	169	5.0	156	22	AA91932	Human protein SEQ
35	168	5.0	240	22	AA91932	Human protein SEQ
36	166.5	4.8	340	22	AA91932	Human protein SEQ
37	160.5	4.3	918	21	AA91932	Human protein SEQ
38	144	4.1	2194	22	AA91932	Human protein SEQ
39	137.5	4.0	468	21	AA91932	Human protein SEQ
40	132	4.0	468	21	AA91932	Human protein SEQ
41	131.5	4.0	468	21	AA91932	Human protein SEQ
42	131.5	4.0	468	21	AA91932	Human protein SEQ
43	131.5	4.0	468	21	AA91932	Human protein SEQ
44	131.5	4.0	468	21	AA91932	Human protein SEQ
45	131.5	4.0	468	21	AA91932	Human protein SEQ

ALIGNMENTS

AA91932

ID AA91932 standard; Protein; 561 AA.

AC AA91932;

DT 11-DEC-1996 (first entry)

XX Phosphatidylinositol-4,5-diphosphate specific phospholipase C.

XX Columbia ecotype; transformed host; expression vector;

XX recombinant production.

XX Arabidopsis thaliana.

XX Key

XX Domain

XX Domain

XX Domain

XX Domain

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XX Domain

Query Match 21.0%; Score 698.5; DB 22; Length 736;
Best Local Similarity 32.2%; Pred. No. 5e-50;

[illegible]

QY	427	WNYGAQWVAQNMOGYGKELWQAFKRGKNGGCGYVLKPOYLLENLPSCGVPEPNTSPRNTT	486
Db	603	wnscgcqvalnftqpgyemlagnrfivngcgylkpaclrqpsdfdepypgprttc-	661
QY	487	LILIKIKVMTTLGWDKAFSKRRHFDLSPDPFTRVIVGVPADEAKWKTSS-VVDNSWAPHW	545
Db	662	--lsiqvlttaqglpklnaekphsivdp--lvrliehgvpadcarqetdyvlnngfnprw	716
QY	546	NEDHEFALCPALALRIEVRDHDSDSDEFEQGTCLPIHEVRDGYRCMQWYDKKG	601
Db	717	gqtlqfqlrapelalvrfvvedydatspndfvqgtlplsslkqgyrhhliskdg	772
RESULT	4		
AAE10440			
ID	AAE10440	standard; Protein; 762 AA.	
XX	AC	AAE10440;	
XX	XX		
DT	10-DEC-2001	(first entry)	
XX	XX		
XX	XX	Novel human phospholipase protein #7.	
KW	KW	Human; novel human protein; NHP; phospholipase protein; phospholipid;	
KW	KW	phospholipase C delta-4; cell activation; signal transduction; cancer;	
KW	KW	drug screening; biological disorder; mental disorder; medical disorder	
XX	XX	gene therapy.	
OS	OS	Homo sapiens.	
PN	PN	WO200168871-A2.	
XX	XX		
PD	PD	20-SEP-2001.	
XX	XX		
PF	PF	13-MAR-2001; 2001WO-US07994.	
XX	XX		
PR	PR	13-MAR-2000; 2000US-0188885.	
PR	PR	15-MAR-2000; 2000US-0189693.	
PA	PA	(LEXI-) LEXICON GENETICS INC.	
XX	XX		
PI	PI	Hu Y, Nepommichy B, Donoho G, Hilbun E, Turner CA, Abuin A;	
PI	PI	Friedrich G, Zambrowicz B, Sands AT;	
XX	XX		
DR	DR	WPI; 2001-582456/65.	
XX	XX	N-PSDB; AAD17564.	
XX	XX		
PT	PT	New polynucleotides encoding human phospholipase protein involved in	
PT	PT	cell activation and signal transduction, useful for drug screening,	
XX	XX	diagnosis and in gene therapy of biological disorders	
PS	PS	Claim 11; Page 41-43; 45pp; English.	
XX	XX		
CC	CC	The present sequence is novel human protein (NHP), phospholipase	
CC	CC	protein. Phospholipases hydrolyse phospholipids and play a key	
CC	CC	role in the cell activation and signal transduction. NHPs share	
CC	CC	structural similarity with animal phospholipases, including phospho-	
CC	CC	lipase C delta-4. NHP oligonucleotides are useful in conjunction with	
CC	CC	polymerase chain reaction (PCR) to screen libraries, isolate clones,	
CC	CC	and prepare cloning and sequencing templates, and alternatively as	
CC	CC	hybridisation probes for screening libraries and assessing gene	
CC	CC	expression patterns. They are used in the identification, selection	
CC	CC	and validation of novel molecular targets for drug discovery, selection	
CC	CC	identification and characterisation of human genomic clones is helpful	
CC	CC	for identifying polymorphisms, determining the genomic structure of a	
CC	CC	given locus/allele and designing diagnostic tests. The microarray	
CC	CC	comprising NHP cDNA is useful for screening collections of genetic	
CC	CC	material from patients having a particular medical condition, which	
CC	CC	is used to identify mutations associated with a particular disease and	
CC	CC	also as diagnostic or prognostic assay. NHP nucleotide sequences are	
CC	CC	useful for drug screening. Nucleotide construct encoding NHP protein	

Db 243 evsdsedsadeideckfklhysngttghv-----esfirkklesllkesqirdekdpdsf 298
 QY 323 SPDLGAT-----STRYSKNDGNDNPKFKYARLITIRLAKHAGT---SMEHRLQVDE 375
 Db 299 tvraillkathegnlahikgspdvkesgk-shgrslmtngfghkktksksysstddee 357
 QY 376 SVKR-----ISLSESK 386
 Db 358 dtqgstqkeggqlrlyrrrrktmkclrelsdlyvvtnsaaqdivddgttgnvlsfsetr 417
 QY 387 LEKVEKWPALVKFTQKNILRVYPAANRVNSNFCTPLAWNYGAQMAVQMGYKELW 446
 Db 418 ahqvqqkseqfmlyngkqitriypsayridsnfnplwagcqilvalnyqsegrmmq 477
 QY 447 QAGCKFKNGCGGVYLPQVLLNLSGVFPNPTS-----PRNTTLIKIKVMTTLGWOKA 502
 Db 478 lnrakfngangnyvlpqgmckg-----tfnpfsgdplpanpkkqllkvisgqqlpkp 532
 QY 503 FSKRHFDLFPDPFFTRVIVGVGPADEAKWTSV-DNSWAPHWNEDEHFAKCPDELALL 561
 Db 533 pdsfmfdrgelidpfveveilegipvdckdqtrrvddngfnpvweetitftvhpmeialv 592
 QY 562 RIEVRHDDSDKDEFEQGTCLPIHEVRDGYR 592
 Db 593 rflvwdhdpigrd-fvgqtrvtvsslvpgyr 622

RESULT 6

AAW81394

ID AAY81394 standard; protein; 756 AA.

AC AAY81394;

DT 19-JUN-2000 (first entry)

DE Rat phospholipase C-delta-1.

XX

KW Phospholipase C-delta-1; rat; PH domain; inositol triphosphate;

KW quantitation; distribution; fluorescent label; hypertension;

KW inflammation; dementia; immunodeficiency; diagnosis; treatment.

XX

OS Rattus sp.

XX

FH Key

FT Domain

FT Location/Qualifiers

FT 1..147

FT /note= "PH domain"

XX

PN WO200011213-A1.

XX

PD 02-MAR-2000.

XX

PF 23-AUG-1999; 99WO-JP04512.

XX

PR 24-AUG-1998; 98JP-0237714.

XX

PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.

XX

PI Hirose K, Takejima H, Iino M;

XX

DR WPI; 2000-224715/19.

XX

PT Fluorescent probe made from phospholipase C-delta and fluorescent

PT substance for simple and accurate quantitation of inositol triphosphate

PT and its distribution in cells, applicable in diagnosis and treatment of

PT e.g. hypertension

XX

PS Claim 11; Page 14-18; 22pp; Japanese.

XX

CC The invention relates to a fluorescent probe comprising phospholipase

CC C-delta (or a portion thereof, such as the PH domain) and a fluorescent

CC substance. The invention also encompasses fusion genes encoding a fusion

CC protein of phospholipase C-delta (or a portion thereof) and a fluorescent

CC protein (e.g. green fluorescent protein, GFP) and methods for

CC quantitating inositol triphosphate concentration and determining the
 CC distribution of inositol triphosphate in cells using the fluorescent
 CC probe. The fluorescent phospholipase C-delta probes of the invention may
 CC be used for simple and accurate quantitation of inositol triphosphate and
 CC its distribution in cells. It is also useful in the diagnosis and
 CC treatment of hypertension, dementia, inflammation and immunodeficiency,
 CC as well as in drug development. The present sequence represents rat
 CC phospholipase C-delta-1.
 XX
 SQ Sequence 756 AA;

Query Match 17.9%; Score 594.5; DB 21; Length 756;
 Best Local Similarity 28.7%; Pred No. 3.3e-41;
 Matches 173; Conservative 96; Mismatches 215; Indels 119; Gaps 16;

QY 32 ERMSAGSLKFLHTEGGVDFTLDQAKQIMERIRKDWKSKFGLASINSDLSKEAFRYLM 91
 Db 226 etlsverlvtfiqhqqreeagpalalslieryeps-----etakaqrmtkdgflmyli 280
 QY 92 NPDLN--GVLHNHVHODMTOPMSHYFIFTGHSNYLTGNQLSSDSDTPIAAALRRGVVV 149
 Db 281 sadgnafslahrsvyqmdqplshylvssshntylledqgtgspsteayiralcgcrcl 340
 QY 150 ELDLPDDKGGMKVTHGNTLTNPVSFQKCVTAIKNNAFETSEYPCVVTIEDHLTSELQGH 209
 Db 341 eldcwdgpnqepiivhytfskilfcvldraidyafkaspyvllslenhcsleqgrv 400
 QY 210 AAEILEQILGDALYPTTDLVPEPPSPESLKRKIIISTK-----PPK 252
 Db 401 marhlraillgdpilldqpildgvttslpspeqlkgkllkgkllgllpaggengseatdvs 460
 QY 253 EYLEACSTQKLAENRNLVEELEKEDKLEQTFAPLEENHILGENTPSLKEVEVLSQKE 312
 Db 461 deveaaamedeav--rsqvqhkpkedkkl-----vpeI----- 492
 QY 313 MSTPAELNSRSPDLSGEATSTRYSKNDGNDNPKHFYARLITIRLAKHAKGTSMEHRLQ 372
 Db 493 -----sdm-----liycks-----vhfg-----gfsspglsgqafye 519
 QY 373 VDESVKRISLSSEKLEKVVVEKWEALVKFTQKNILRVYPAANRVNSNFCTPLAWNYGAQ 432
 Db 520 m-----asfsearalrllgesngfvrhmvscslriypagwtddsnyspvmwngq 573
 QY 433 MYAQNMQYKELWQAFKFGKNGCGGVYLPQVLLNLSGVFPNTPSPRNTTLI----- 488
 Db 574 ivalnfqtpgemdyllgcfdnggcgyvlpafld-----pntfnsraltqgp 624
 QY 489 -----LKIVMTTLGWDKAFSRKHFDLFPDPFFTRVIVV--GVPADEAKWTSYV--DN 539
 Db 625 wrperlrviisgqqlpkv-nknksivdp-----kvivelhgvgrdtgsqtavittn 678
 QY 540 SWAPHWNEDEHFAKCPDELALLRIEVRHDDSDKDEFEQGTCLPIHEVRDGYRCHQWMDK 599
 Db 679 gfnprwmefefevtpdialvrfmvedyssekndfiggstipwnslkqgyrhvhlslk 738
 QY 600 KGN 602
 Db 739 ngd 741

RESULT 7

AAW01596

ID AAW01596 standard; Protein; 1096 AA.

XX AAW01596;

XX AC

XX DT 17-MAR-1997 (first entry)

XX

DE Inositol-1,4,5-triphosphate binding protein.

XX

KW IP-3; inositol-1,4,5-triphosphate; phospholipase C-delta 1;

KW drug testing; screening; diagnostic; cancer; inflammatory disease;

'Sun Jul 28 10:34:35 2002

728 iisgnqfpgkacag--dvidp---yvcvhihpadcseqrtktvqnsdnpifdet 782
 549 HEFALKCPALLRIEVRDHDHDDSKDEFEGTCLPIHEVRDGYRCMOMYDKGNVLKGV 608
 783 fefqvnlpeltnvrfvild-ddyigdefigtytipeclpgyrvhprsvfgdimehvt 841
 609 MLFH 612
 842 lfvh 845

RESULT 8
 AAB94673
 ID AAB94673 standard; Protein; 677 AA.
 AC AAB94673;
 DT 26-JUN-2001 (first entry)
 XX Human protein sequence SEQ ID NO:15618.
 DE Human; primer; detection; diagnosis; antisense therapy; gene therapy.
 KW Homo sapiens.
 XX EPI074617-A2.
 PN 07-FEB-2001.
 PD 28-JUL-2000; 2000EP-0116126.
 XX 29-JUL-1999; 99JP-0248036.
 PR 27-AUG-1999; 99JP-0300253.
 PR 11-JAN-2000; 2000JP-0118776.
 PR 02-MAY-2000; 2000JP-0183767.
 PR 09-JUN-2000; 2000JP-0241899.
 XX (HELI-) HELIX RES INST.
 PA Ota T, Isogai T, Mishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 WPI; 2001-318749/34.

Claim 8; SEQ ID 15618; 2537pp + CD ROM; English.

The present invention describes primer sets for synthesizing 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesizing polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.

Full-length cDNAs defined in the specification, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.

KW tumour; circulatory organ disease.
 XX Rattus sp.
 XX JF08266283-A.
 XX 15-OCT-1996.
 XX 31-MAR-1995; 95JP-0075876.
 XX 31-MAR-1995; 95JP-0075876.
 XX (HIRA/) HIRATA M.
 XX (MITK) MITSUI TOATSU CHEM INC.
 XX WPI; 1996-512670/51.
 XX N-PSDB; AAT58225.
 XX Structural gene encoding protein capable of binding with inositol-1,4,5-trisphosphate - useful for creation of drugs and diagnostics for, e.g. circulatory organ diseases, inflammatory diseases, etc.
 XX Claim 2; Page 6-11; 13pp; Japanese.
 XX This sequence is a 130 kD protein capable of binding inositol-1,4,5-trisphosphate (IP-3). The protein has approx. 38.2 percent homology with phospholipase C-delta 1 (PLC-delta 1). The DNA (AAT58225) encoding it, is important for the creation of drugs and diagnostic agents for various diseases, e.g. circulatory organ, inflammatory and nerve diseases, malignant tumours and cancers.
 XX Sequence 1096 AA;

Query Match 16.8%; Score 559; DB 17; Length 1096;
 Best Local Similarity 28.3%; Pred. No. 6e-38; Indels 100; Gaps 16;
 Matches 171; Conservative 95; Mismatches 238;
 QY 27 IYSENERMAGLLFLHTEQGDVDFDLDAAQIMER--IRKDWK-KSFGLANSLSL 83
 DB 324 lskneyidandlmifveqgthvtdmclidrryelsedgrqkf-----lai 375
 QY 84 EAFKRYLMP--DLNGLVHNVHQMTPMASHYFIFTGNSYLTGNLSDDSDTPATAA 141
 DB 376 dgftqyllspedifpeqkkaqdmtpqplshyinashtyiledqfgrpaddingyva 435
 QY 142 LRGRVVRVLDLPDCKGGMKVTGNLTNPVSFOKCVTAIKNNAPFTSEYPCVVTIEDH 201
 DB 436 lkmgrsiedlvdsdgdndepilcnrnmamllsfrsvlevinkfafvaseyplilclgnh 495
 QY 202 LTSELOGHAAEILLEQLGDALYPTTDDALVEFPSPESIKRKTIITSTKPPKEYLEACSTQ 261
 DB 496 cslpqqrvmvqgmkvfngklyteaplsesylpspekikhmilvkgk----- 543
 QY 262 KLANENRLVELEKEDKLEOTTTFAPLEENHILGENTPSLRKEVEYLSOKEMSTPAELNS 321
 DB 544 klpsesdllegevdede-----eaemr 567
 QY 322 RSPDLGEATSTRYSKSDNGNDNPKHKFYARLIT--IRLAKHAKGTSMERHQVDSYKR 379
 DB 568 r-----vsgdyngedqkhiwlcrlsdlvsicksyqydfelsmktqnywei 613
 QY 380 ISLSSEKLEKVEKWEALYKFTOKNLTIRVYPAANRVNNSNFCPTLAWNYGAQVQNNQ 439
 DB 614 cfsfslarlaneyedfnynkklfsvypsamridsnlppqdfwncgcqivamnfq 673
 QY 440 GYGKELWQAFKFGKNGCGGVLPK-----QYLLNLSGVPFNPFTSPRNTTLILKIK 492
 DB 674 tpgpmldlhtgfwlqngcgylrpslmrdevsyfsantkgivp--gvsp-----llhlk 727
 QY 493 VMTTLGWDK--AFSKRHFDLSPDPDFTRVIVGVPADEAKWKTSSV--DNSWAPHNED 548

PR	06-OCT-1999;	99US-01578665.
PR	07-OCT-1999;	99US-01580209.
PR	08-OCT-1999;	99US-01582323.
PR	12-OCT-1999;	99US-01583669.
PR	13-OCT-1999;	99US-01585293.
PR	13-OCT-1999;	99US-01592294.
PR	13-OCT-1999;	99US-01592395.
PR	14-OCT-1999;	99US-01593359.
PR	14-OCT-1999;	99US-01593330.
PR	14-OCT-1999;	99US-01595331.
PR	14-OCT-1999;	99US-01596637.
PR	18-OCT-1999;	99US-01596368.
PR	21-OCT-1999;	99US-01595864.
PR	21-OCT-1999;	99US-0160741.
PR	21-OCT-1999;	99US-01607667.
PR	21-OCT-1999;	99US-01607668.
PR	21-OCT-1999;	99US-01607770.
PR	22-OCT-1999;	99US-01608814.
PR	22-OCT-1999;	99US-01608815.
PR	22-OCT-1999;	99US-01609081.
PR	22-OCT-1999;	99US-01609080.
PR	25-OCT-1999;	99US-01609089.
PR	25-OCT-1999;	99US-01614004.
PR	25-OCT-1999;	99US-01614005.
PR	26-OCT-1999;	99US-01614006.
PR	26-OCT-1999;	99US-01613599.
PR	26-OCT-1999;	99US-01613660.
PR	28-OCT-1999;	99US-01613661.
PR	28-OCT-1999;	99US-01619200.
PR	28-OCT-1999;	99US-0161992.
PR	29-OCT-1999;	99US-0161993.
PR	29-OCT-1999;	99US-01621442.

2:

RESULT 10
AAE13101

AAE13101:

DE Human phospholipase C family member, 16836 protein.
XX

Human; phospholipase C; PLC; 16836 protein; cellular disorder; sarcoma; carcinoma; metastatic disorder; leukaemia; bone disorder; osteoporosis; haematopoietic neoplastic disorder; sarcoidosis; Alzheimer's disease; Parkinson's disease; brain disorder; reproductive disorder; gonorrhoea; teratoma; immune disorder; rheumatoid arthritis; cardiovascular disorder; Grave's disease; atherosclerosis; cardiomyopathy; anorexia nervosa; obesity; cachexia; lipid disorder; diabetes; hepatocellular carcinoma; viral disease; gene therapy; cytostatic; osteopathic; immunosuppressive; neuroprotective; dermatological; ophthalmological; neotropic; vasotropic;

Sun Jul 28 10:34:35 2002

KW hypotensive; anticonvulsant; antibacterial; tuberculostatic; virucide;
 XX vulnary; anorectic.
 OS Homo sapiens.
 XX Location/Qualifiers
 FH 35..338
 FT /label= RasGEF domain
 FT /note= "Ras guanine nucleotide exchange factor domain"
 FT 900..1048
 FT /label= PI-PLC-X domain
 FT /note= "Phosphatidylinositol-specific
 FT phospholipase C-X domain"
 FT 1171..1184
 FT /label= PI-PLC-Y domain
 FT /note= "Phosphatidylinositol-specific
 FT phospholipase C-Y domain"
 FT 1261..1353
 FT /label= PI-PLC-Z domain
 FT /note= "Phosphatidylinositol-specific
 FT phospholipase C-Z domain"
 FT 1378..1460
 FT /label= C2 domain
 FT 1640..1745
 FT /label= RA domain
 FT /note= "Ras association domain"
 XX WO200175121-A2.
 XX 11-OCT-2001.
 XX 30-MAR-2001; 2001WO-US10273.
 XX 31-MAR-2000; 2000US-193921P.
 XX (MILL-) MILLENNIUM PHARM INC.
 XX Meyers RA, Hunter JJ;
 XX WPI: 2001-662975/76.
 XX N-PSDB; AAD21290.
 XX New polypeptide for controlling cellular proliferative and/or
 XX differentiative disorders such as lung, breast or colon cancers,
 XX comprises a member of human phospholipase C family, referred to as
 XX 16836 -
 XX Claim 9; Fig 1; 148pp; English.
 XX The present invention relates to novel human phospholipase C (PLC)
 XX family members, designated as 16836 and polynucleotides encoding
 XX them. 16836 sequences are useful for treating cellular proliferative
 XX and/or differentiative disorders such as carcinoma, sarcoma, metastatic
 XX disorders or haematopoietic neoplastic disorders (e.g. leukaemias)
 XX which arise from myeloid, lymphoid or erythroid lineages or their
 XX precursor cells. They are also useful for treating bone disorders
 XX (e.g. osteoporosis, sarcoidosis), brain disorders (e.g. Alzheimer's
 XX disease, Parkinson's disease), reproductive disorders (e.g. gonorrhoea,
 XX teratoma), immune disorders (e.g. rheumatoid arthritis, Grave's disease),
 XX cardiovascular disorders (atherosclerosis, cardiomyopathies) or diseases
 XX of metabolic imbalance such as obesity, anorexia nervosa, cachexia,
 XX lipid disorders and diabetes. 16836 molecules of the invention are
 XX used to treat disorders associated with an accumulation in the liver
 XX of fibrous tissue, such as that resulting from an imbalance between
 XX production and degradation of the extracellular matrix accompanied
 XX by the collapse and condensation of preexisting fibers. They are
 XX useful as markers for precursors or predisposition of disorders
 XX or disease states, as markers of drug activity or as markers of the
 XX pharmacogenomic profile of a subject. Modulators of 16836 activity
 XX could be used to control viral diseases. They are used in the treatment
 XX and/or diagnosis of virus-associated carcinoma, especially hepatocellular
 XX cancer. 16836 sequences are also used in gene therapy. The present
 XX sequence is phospholipase C (PLC) family member, 16836 protein from

CC human.
 XX Sequence 1809 AA;
 SQ Query Match 15.3%; Score 508.5; DB 22; Length 1809;
 Best Local Similarity 24.1%; Pred. No. 2.5e-33; Indels 165; Gaps 21;
 Matches 167; Conservative 121; Mismatches 240;
 QY 38 GLLK---FLHTEQGVDFTLDDAKQIMERIRKDKKSKFGLASINSLSKAEAFKRYLMNPD 94
 DB 832 gilqlndflvcqge-hctydeillsiqk-----fepsismch-qgllmsfegfarflmdke 885
 QY 95 LNCVLHNVVHQ---DMTPQMSHYFIFTGNSYLTGNQLSSDSDPIAAALRRGVVVE 150
 DB 886 -faskndesqenikelplisyvyyiesshntyltghlkgessvelysqvllqcrsv 944
 QY 151 LDLPDDKGGKMTGNITLNPVFOKVTAKNNAPFTSEYPCVCTIEDHTSELOGHA 210
 DB 945 ldcwdgdgmpliyhgtlttkipfkveveaidrsafinsdplliisienhcsalpqqrkm 1004
 QY 211 AEILEOILGDALYPTTDDALVE-----FSPESLKRKIIISTK-----PPREYLE 256
 DB 1005 aelfktvfgekl---vtklfetsddpmlpspdqirrkvllknkklkahqtpvdilk 1060
 QY 257 ACSTQKLAMENR-----NLVELEKEDLEQTTFAPEENHILGENTP-----299
 DB 1061 qkahqlasmqvgayngnanpranneeedeedy-dyeslsddnil-edrpenksc 1118
 QY 300 -----SLRKEVEVLSQKEMSTPAELNSRSPDGLGEATSTRYSKSNQDNDNP-----345
 DB 1119 ndklqfeyneeipkrirkkadsnckgkydmeelgeefyldqnkkesqlapelsdiviy 1178
 QY 346 -KHFYARLTIRLAKHAKGTSMEHLQV-----SLESKLEKVEKWEALVKFTQKNILRVYPA 413
 DB 1179 eqavkfpglscinasgssrgkrsksifgnnpgrmspgetasfnktsksscegirqt 1238
 QY 374 -DESVKRI-----SLESKLEKVEKWEALVKFTQKNILRVYPA 413
 DB 1239 weessspnpttsisairtpkcyhsslnenaakrircrysqklqtacqllttypaa 1298
 QY 414 NRVNSNFCPTLANNYGAVQMAQNMQYGRKELMQAFKFGKNGCGYVLPKPYLLE-NLP 472
 DB 1299 tridsnnpnplmfwhlgqlvalnyqddplphlnaamfeangcgvykppvldkncp 1358
 QY 473 SGVPNPSPRNTLILKIKVMTLGDWKAFAKSRHDFLSPDPDFTRVI-----521
 DB 1359 myqkfsp-----erldsmdpavysltivsggnvcpsnsm 1394
 QY 522 -----VVGVPADAEAKWKTSSVD-NSWAPHWNEDHEFALKCPELALLRIEVRDHD 572
 DB 1395 gspcievdivgmpldschfrtkphrntlnpmwneqflhvfhedlvlfavvennsa 1454
 QY 573 KDEFEGQCTCLPHEVRDGRCHQMDKKGNVLK 605
 DB 1455 ---vtadriiplkalkrgyrhqlrnlhnevie 1484
 RESULT 11
 ID AAM80177 standard; Protein; 1058 AA.
 XX AAM80177;
 XX AAM80177;
 XX 06-NOV-2001 (first entry)
 XX Human protein SEQ ID NO 3823.
 DE Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 XX vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorder; arthritis; inflammation.
 XX

324	PSDLGEATSTRYSKSDNGDNDKHPKY	-----ARLIT-----IRLAKHAKGTSMEHR	370
499	pspgageatdesdaddddckksmdegtagesamateenslnvnylqpvkfesfeis	-----ARLIT-----IRLAKHAKGTSMEHR	370
371	LQVDESVRKISLSBSKLEKVKWEPEALVKFTQTNILRVVPAANRVSSNFCPTLANNYG	-----ARLIT-----IRLAKHAKGTSMEHR	370
559	kkrrksfemsfvctkgleqltkspvefveynkqlsriypkqtrvdsnmpqlfwnag	-----ARLIT-----IRLAKHAKGTSMEHR	370
431	AQMVAQNMQGYGKELWQAFKFGKNGCGGYLKPQYL	-----LENLPSGVPPNPPT	480
619	cqmvalnfqmtldamqnmmyeayngksgyrlkpefirrrdkhdfpftgevgdivan--	-----LENLPSGVPPNPPT	480
481	SPRNTLILKTVMTTLGWDAKSKRHFOLFSPDFETRIVVGVPADEA-----KWKTSV	-----LENLPSGVPPNPPT	480
677	-----tlsvkllsgfisdhkvtyvevdmf	-----LENLPSGVPPNPPT	480
537	VDNSWAPHNEDHEFALK--CPELALLRIVERDHDSDKDFEQTCCLPIHEVRDGYRCM	-----LENLPSGVPPNPPT	480
719	qgnavnpveeeipvfkkkvvliptlaciariav--yeegqg--fighriilpvqairpgyhi	-----LENLPSGVPPNPPT	480
595	QMTDKKGNVL	-----LENLPSGVPPNPPT	480
775	clnrnqnpl	-----LENLPSGVPPNPPT	480

475 diangistglhrslgaggahgengenvrkfkegllfykdpvdkswmlyqfvl 534
 255 -----LEACS-----TOKLAWEN----- 267
 535 thqeliysseinearnsgnsddfglssscslnsnmqkqkdtasandehlfgenwfngkl 594
 268 ---RNLVELEKEDK---LEQTTPAP----- 287
 595 eggrkeaddllkkyhfgdgtflvresatfvdygysifwrrnphrhczikiklhengisyk 654
 288 ---LEENH-----ILGENTPSLKE----- 304
 655 yivenfvfdslslylvyrknmlrsesfllkepvqpkkhedqewfhpnttkeaqg 714
 305 -----VEVLSOKEMSTPAELN 320
 715 lyreigslvrpsvgsinafvstlnrkikhrimqegrlgyldtmfesslvsliny 774
 321 SRSP-----SDUGEXTSTFYKSKNDGN-----DN----- 344
 775 trnplyrnklshpvsqellrqalaeaaqdgshgghdngasnyngsnleenvtckalys 834
 345 -----PKHF-----KYARLITIRL-AKHAK----- 363
 835 ykxnpdelsfkhaitnvrdrnmwagdygmkhkhlpnykvkvidstetdedsline 894
 364 -GP-----SME-----HRLQVD-----ESVKRI- 380
 895 egtgdrtslfagavalfesndpgllfklqitqtmqnpfvigdnqetayewikaq 954
 381 -----SLESKLEK-V 390
 955 ealliasqlaserkkertarvakemsdlilyfrsvfrehswlfqemssfpetkaekqf 1014
 391 VEKWEALVKFTQKILNLRVYPAANRVNSNFCPTLANNYGAQVNAQNMOCYKELWQAF 450
 1015 fqqtqglfslhrnqlsvrpkgrldssnfpmpfwngsqmialnyqgkamqinda 1074
 451 KFKNGCGGVYLVKPOYLENLPSPVPNPSPRNTTLILKIKVMTTTLGWDAKAFSKRHF 510
 1075 kfrnngcgylkpsfmsd-----sinpnpclcdgl-sevkvslr-----iaarh-- 1121
 511 F-----SPDEFRTVWGVPADE-AKWTSTVDNSWAPWNEDEHFFALKCPCELALLRIE 564
 1122 frggksnnpqiv--veligasfdgvkytkvngfnpvnescefnvnpqfailrfe 1179
 565 VRDHDDSDKDEFEQOTCLPIHEVRDGYRCMQYDKKGNVLKGVLMFLHFQKCKT 619
 1180 vqdedmaethiaqacpctcirgyrsvlrnlkfseelelssllinikianvt 1234
 RESULT 14
 ABB60755 standard; Protein; 1312 AA.
 ID ABB60755 standard; Protein; 1312 AA.
 AC ABB60755;
 DT 26-MAR-2002 (first entry)
 XX Drosophila melanogaster polypeptide SEQ ID NO 9057.
 DE Drosophila melanogaster polypeptide; cell signalling; insecticide;
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 XX Drosophila melanogaster.
 OS Drosophila melanogaster.
 PN WO2001/1042-A2.
 PD 27-SEP-2001.
 PF 23-MAR-2001; 2001WO-09231.

23-MAR-2000; 2000US-191637P.
 11-JUL-2000; 2000US-0614150.
 (PEKE) PE CORP NY.
 Venter JC, Adams M, Li PWD, Myers EM;
 WPI: 2001-656860/75.
 N-FSDB; ABL04858.
 New isolated nucleic acid detection reagent for detecting 1000 or more
 genes from Drosophila and for elucidating cell signalling and cell-cell
 interactions -
 Disclosure; SEQ ID NO 9057; 21pp + Sequence Listing; English.
 The invention relates to an isolated nucleic acid detection reagent is
 capable of detecting 1000 or more genes from Drosophila. The invention and
 useful in developmental biology and in elucidating cell signalling of
 cell-cell interactions in higher eukaryotes for the development of
 insecticides, therapeutics and pharmaceutical drugs. The invention
 discloses genomic DNA sequences (AB116176-AB130511), expressed DNA
 sequences (AB01840-AB116175) and the encoded proteins
 (AB57737-AB72072).
 The sequence data for this patent did not form part of the printed
 specification, but was obtained in electronic format directly from WIPO
 at ftp.wipo.int/pub/published_pct_sequences.
 Query Match 14.0%; Score 464.5; DB 22; Length 1312;
 Best Local Similarity 25.5%; Pred. No. 8e-30; Indels 155; Gaps 24;
 Matches 178; Conservative 97; Mismatches 268; Indels 155; Gaps 24;
 9 GCPKGDPPQDLVG-----EVFTIY-----SENER-----MSAEGLLKFLH 44
 193 tglpsgkvdslsvskfgedfynlykyltqrseverfslsvgnskrkcmiaqlvelfn 252
 45 TEQGD-----VDFTLDDAKOIMERIRKDKMKSFGLSINSDLSKAFKRYKILNPDNLGVL 99
 253 ktqqrprineillypanparakellqyepnkfn--aqgqlslgdlfrylmgdd-npm 309
 100 HNV---VHODTQPMSHYFTTGHNSYLTGNLSNDSSTDPFAAALRGVRYVVELDLPD 156
 310 apskldicdmqpmshyfnsshtytlqhtkqssvlyrqcllagrcvclafwng 369
 157 DKGMKVTHGNVLTNPVSFQKCVTAIKNNAFTSEYPCVCTTIEDHLTSELQGHAAETLEQ 216
 370 rteeprvghytrfvepfakdvleaaesaktseypvllsfenhcnpqakianycr 429
 217 ILGDALYYP-----FTDALVEFSPESLKRKILITKPKKEY----- 254
 430 ifgdmlldkpladshplepmdlppamllrklilknkhhhhhhhhhhhhhhhhhhhhhhhh 489
 255 -----LEACSTQKLM-----ENRNLVEELEKEDKLEOTFA----- 289
 490 nmklitansvdakaqqvglsashedgvttrstangdvatgtgsaagtaghaplqql 549
 290 -----ENHILGENTPSLRKEVE-----VLSOKEMSTPAELNSRSPSLDGE 329
 550 rgsksdgtsgsdssssedeslnttpnlpsgnepppekaqketeaaisa----- 601
 330 ATSTRYSKNDGNDNPKHFYARLITIRLAKHAGTSMHEHLQVDESVKRISLSKLEK 389
 602 --lrvnyvq-----plhf-----ssfenaekknrcyemssfdeqatt 636
 390 VVEKWEALVKFTQKILNLRVYPAANRVNSNFCPTLANNYGAQVNAQNMOCYKELWQAF 449
 637 llkerpiefvnyukhqlsrsrvpagtrfdssnfmpqlfwagcqlvalnfqldlamqnl 696
 450 GKFKNGCGGVYLVKPOYLENLPSPVPNPSPRNTTLILKIKVMTTTLGWDAKAFSKRHF 509

us-09-828-447-12.rag

Db 637 gifeynarsyglkpefmrrsdrldpfaestvdg--iagtvsvtlsgqfldtkr-- 751

Qy 510 LFSPDPFFTRVIVGVGVPAD--EAKWTSV-DNSWAPHWNEDHEFALK---CPELALLRI 563

Db 752 -----actfvevdmglpadtrvkrkfrktvrdngmnplydee-pivfkkvlpelasiiri 806

Qy 564 EYRDHDDSKDFEQQCLPHEVRDGYRCMQMDKKG 601

Db 807 aa-yeeggk-llghrvlpvgicpgyrhvnlsevg 840

RESULT 15

AAG25436

ID AAG25436 standard; Protein; 178 AA.

AC AAG25436;

XX XX

DT 17-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO.: 29499.

XX Protein identification; signal transduction pathway; metabolic pathway;

KW hybridisation assay; genetic mapping; gene expression control; Promoter;

KW termination sequence.

XX Arabidopsis thaliana.

OS EP1033405-A2.

FN XX

PD XX

XX XX

PF 06-SEP-2000.

XX XX

XX 25-FEB-2000; 2000EP-0301439.

PR 03-MAR-1999; 99US-0121825.

PR 09-MAR-1999; 99US-0123180.

PR 23-MAR-1999; 99US-0123548.

PR 29-MAR-1999; 99US-0125788.

PR 29-MAR-1999; 99US-0126264.

PR 01-APR-1999; 99US-0126785.

PR 06-APR-1999; 99US-0127462.

PR 16-APR-1999; 99US-0128234.

PR 18-APR-1999; 99US-0128714.

PR 19-APR-1999; 99US-0129845.

PR 21-APR-1999; 99US-0130077.

PR 23-APR-1999; 99US-0130510.

PR 23-APR-1999; 99US-0130891.

PR 30-APR-1999; 99US-0131449.

PR 30-APR-1999; 99US-0132048.

PR 04-MAY-1999; 99US-0132407.

PR 05-MAY-1999; 99US-0132484.

PR 06-MAY-1999; 99US-0132485.

PR 07-MAY-1999; 99US-0132486.

PR 11-MAY-1999; 99US-0132487.

PR 14-MAY-1999; 99US-0134256.

PR 14-MAY-1999; 99US-0134218.

PR 14-MAY-1999; 99US-0134219.

PR 14-MAY-1999; 99US-0134221.

PR 18-MAY-1999; 99US-0134370.

PR 19-MAY-1999; 99US-0134768.

PR 20-MAY-1999; 99US-0134941.

PR 21-MAY-1999; 99US-0135124.

PR 24-MAY-1999; 99US-0135353.

PR 25-MAY-1999; 99US-0135629.

PR 27-MAY-1999; 99US-0136021.

PR 28-MAY-1999; 99US-0136392.

PR 01-JUN-1999; 99US-0136782.

PR 03-JUN-1999; 99US-0137222.

PR 04-JUN-1999; 99US-0137528.

PR 07-JUN-1999; 99US-0137502.

PR 08-JUN-1999; 99US-0137724.

PR 99US-0138094.

PR 10-JUN-1999; 99US-0138540.

PR 10-JUN-1999; 99US-0138847.

PR 14-JUN-1999; 99US-0139119.

PR 16-JUN-1999; 99US-0139452.

PR 17-JUN-1999; 99US-0139453.

PR 18-JUN-1999; 99US-0139492.

PR 18-JUN-1999; 99US-0139454.

PR 18-JUN-1999; 99US-0139455.

PR 18-JUN-1999; 99US-0139456.

PR 18-JUN-1999; 99US-0139457.

PR 18-JUN-1999; 99US-0139458.

PR 18-JUN-1999; 99US-0139459.

PR 18-JUN-1999; 99US-0139460.

PR 18-JUN-1999; 99US-0139461.

PR 18-JUN-1999; 99US-0139462.

PR 18-JUN-1999; 99US-0139463.

PR 18-JUN-1999; 99US-0139750.

PR 21-JUN-1999; 99US-0139763.

PR 22-JUN-1999; 99US-0139817.

PR 23-JUN-1999; 99US-0139899.

PR 23-JUN-1999; 99US-0140353.

PR 24-JUN-1999; 99US-0140354.

PR 28-JUN-1999; 99US-0140695.

PR 28-JUN-1999; 99US-0140823.

PR 30-JUN-1999; 99US-0140991.

PR 01-JUL-1999; 99US-0141287.

PR 01-JUL-1999; 99US-0141842.

PR 02-JUL-1999; 99US-0142154.

PR 06-JUL-1999; 99US-0142055.

PR 08-JUL-1999; 99US-0142380.

PR 09-JUL-1999; 99US-0142803.

PR 12-JUL-1999; 99US-0142920.

PR 13-JUL-1999; 99US-0142977.

PR 14-JUL-1999; 99US-0143542.

PR 15-JUL-1999; 99US-0143624.

PR 16-JUL-1999; 99US-0144005.

PR 16-JUL-1999; 99US-0144085.

PR 19-JUL-1999; 99US-0144085.

PR 19-JUL-1999; 99US-0144325.

PR 19-JUL-1999; 99US-0144331.

PR 19-JUL-1999; 99US-0144332.

PR 19-JUL-1999; 99US-0144333.

PR 19-JUL-1999; 99US-0144334.

PR 20-JUL-1999; 99US-0144335.

PR 20-JUL-1999; 99US-0144352.

PR 21-JUL-1999; 99US-0144632.

PR 21-JUL-1999; 99US-0144684.

PR 21-JUL-1999; 99US-0144814.

PR 21-JUL-1999; 99US-0145086.

PR 22-JUL-1999; 99US-0145088.

PR 22-JUL-1999; 99US-0145087.

PR 22-JUL-1999; 99US-0145087.

PR 22-JUL-1999; 99US-0145089.

PR 23-JUL-1999; 99US-0145192.

PR 23-JUL-1999; 99US-0145145.

PR 23-JUL-1999; 99US-0145218.

PR 26-JUL-1999; 99US-0145224.

PR 27-JUL-1999; 99US-0145276.

PR 27-JUL-1999; 99US-0145913.

PR 27-JUL-1999; 99US-0145918.

PR 28-JUL-1999; 99US-0145919.

PR 02-AUG-1999; 99US-0145951.

PR 02-AUG-1999; 99US-0146386.

PR 02-AUG-1999; 99US-0146388.

PR 03-AUG-1999; 99US-0146388.

PR 04-AUG-1999; 99US-0147038.

PR 04-AUG-1999; 99US-0147204.

PR 05-AUG-1999; 99US-0147302.

PR 05-AUG-1999; 99US-0147192.

PR 06-AUG-1999; 99US-0147260.

PR 06-AUG-1999; 99US-0147303.

PR 09-AUG-1999; 99US-0147416.

PR 09-AUG-1999; 99US-0147493.

PR 09-AUG-1999; 990S-0147935.
PR 10-AUG-1999; 990S-0148171.
PR 11-AUG-1999; 990S-0148319.
PR 12-AUG-1999; 990S-0148341.
PR 13-AUG-1999; 990S-0148565.
PR 16-AUG-1999; 990S-0148684.
PR 17-AUG-1999; 990S-0149368.
PR 18-AUG-1999; 990S-0149426.
PR 20-AUG-1999; 990S-0149722.
PR 20-AUG-1999; 990S-0149723.
PR 20-AUG-1999; 990S-0149929.
PR 23-AUG-1999; 990S-0149902.
PR 23-AUG-1999; 990S-0149930.
PR 25-AUG-1999; 990S-0150566.
PR 26-AUG-1999; 990S-0150884.
PR 27-AUG-1999; 990S-0151065.
PR 27-AUG-1999; 990S-0151066.
PR 27-AUG-1999; 990S-0151080.
PR 30-AUG-1999; 990S-0151303.
PR 31-AUG-1999; 990S-0151438.
PR 01-SEP-1999; 990S-0151930.
PR 07-SEP-1999; 990S-0152363.
PR 10-SEP-1999; 990S-0153070.
PR 13-SEP-1999; 990S-0153758.
PR 15-SEP-1999; 990S-0154018.
PR 16-SEP-1999; 990S-0154039.
PR 20-SEP-1999; 990S-0154779.
PR 22-SEP-1999; 990S-0155139.
PR 23-SEP-1999; 990S-0155486.
PR 24-SEP-1999; 990S-0155659.
PR 28-SEP-1999; 990S-0156458.
PR 29-SEP-1999; 990S-0156596.
PR 04-OCT-1999; 990S-0157117.
PR 05-OCT-1999; 990S-0157753.
PR 06-OCT-1999; 990S-0157865.
PR 07-OCT-1999; 990S-0158029.
PR 08-OCT-1999; 990S-0158232.
PR 12-OCT-1999; 990S-0158369.
PR 13-OCT-1999; 990S-0159293.
PR 13-OCT-1999; 990S-0159294.
PR 13-OCT-1999; 990S-0159295.
PR 14-OCT-1999; 990S-0159329.
PR 14-OCT-1999; 990S-0159330.
PR 14-OCT-1999; 990S-0159331.
PR 14-OCT-1999; 990S-0159637.
PR 14-OCT-1999; 990S-0159638.
PR 18-OCT-1999; 990S-0159584.
PR 21-OCT-1999; 990S-0160741.
PR 21-OCT-1999; 990S-0160767.
PR 21-OCT-1999; 990S-0160768.
PR 21-OCT-1999; 990S-0160770.
PR 21-OCT-1999; 990S-0160814.
PR 21-OCT-1999; 990S-0160815.
PR 22-OCT-1999; 990S-0160980.
PR 22-OCT-1999; 990S-0160981.
PR 22-OCT-1999; 990S-0160989.
PR 25-OCT-1999; 990S-0161404.
PR 25-OCT-1999; 990S-0161405.
PR 25-OCT-1999; 990S-0161406.
PR 26-OCT-1999; 990S-0161359.
PR 26-OCT-1999; 990S-0161360.
PR 26-OCT-1999; 990S-0161361.
PR 28-OCT-1999; 990S-0161920.
PR 28-OCT-1999; 990S-0161922.
PR 28-OCT-1999; 990S-0161993.
PR 29-OCT-1999; 990S-0162142.

Query Match 12.9%; Score 430; DB 21; Length 178;
Best Local Similarity 47.5%; Pred No. 3e-28;
Matches 84; Conservative 26; Mismatches 63; Indels 4; Gaps 2;

QY 433 MVAQNMQYGGKELMQAFKFGKGGCVYVLPQYLLLENLPSCGFNP--TSPRNTTLIK 490

Db 1 mvafnmgygrslwlmggmfrangcggyikkpdlillksgsdsdldfpkatlpvkt--lr 58
QY 491 IKVMTTLGWDKAFSKRHFDLFSPPDFTRIVVGVPADEAKWKTSVVDNSKAPHWNEDHE 550
Db 59 vtvmgegwyfdfrthfdgysppdytrvgiagvgdvmkktktledhwpawdevfe 118
QY 551 FALKCPALALRIEVRDHDSDKDEFEQTCPLPIHEVRDGYRCMQYDKRGNVLKG 607
Db 119 fpltpelallrlvheymsekddfgqtcplpwelsegirafplhsrkgekyksv 175

Search completed: July 26, 2002, 17:23:18
Job time: 4641 sec

Result No.	Score	Query Match %	Length	DB	ID	Description
1	409.5	12.3	1290	1	US-08-138-641-2	Sequence 2, Appli
2	409.5	12.3	1290	1	US-08-138-133-2	Sequence 2, Appli
3	123.5	3.7	573	4	US-08-235-836-112	Sequence 112, Appli
4	120	3.6	2482	1	US-08-338-254-6	Sequence 6, Appli
5	120	3.6	3248	1	US-08-333-700-1	Sequence 1, Appli
6	120	3.6	3248	5	PCT-US95-16216-1	Sequence 1, Appli
7	115	3.5	904	4	US-09-198-484-2	Sequence 2, Appli
8	113.5	3.4	834	1	US-07-977-434-8	Sequence 8, Appli
9	113.5	3.4	834	1	US-08-458-819-8	Sequence 8, Appli
10	113.5	3.4	834	5	PCT-US91-07035-8	Sequence 8, Appli
11	107	3.2	640	3	US-09-026-343-2	Sequence 2, Appli
12	104.5	3.1	834	1	US-07-377-434-10	Sequence 10, Appli
13	104.5	3.1	834	1	US-08-073-384C-6	Sequence 6, Appli
14	104.5	3.1	834	1	US-08-254-359A-6	Sequence 6, Appli
15	104.5	3.1	834	1	US-08-384-490-31	Sequence 31, Appli
16	104.5	3.1	834	1	US-08-483-043-6	Sequence 6, Appli
17	104.5	3.1	834	1	US-08-459-383-31	Sequence 31, Appli
18	104.5	3.1	834	1	US-08-458-819-10	Sequence 10, Appli
19	104.5	3.1	834	1	US-08-481-238-6	Sequence 6, Appli
20	104.5	3.1	834	2	US-08-471-066B-6	Sequence 6, Appli
21	104.5	3.1	834	2	US-08-484-955-6	Sequence 6, Appli
22	104.5	3.1	834	2	US-08-757-653-6	Sequence 6, Appli
23	104.5	3.1	834	2	US-08-599-491-6	Sequence 6, Appli
24	104.5	3.1	834	2	US-08-756-386-6	Sequence 6, Appli
25	104.5	3.1	834	2	US-08-823-516-6	Sequence 6, Appli
26	104.5	3.1	834	3	US-08-682-853A-6	Sequence 6, Appli
27	104.5	3.1	834	3	US-08-759-038-6	Sequence 6, Appli

us-09-828-447-12.ra1

Sun Jul 28 10:34:35 2002

APPLICANT: MACLEOD, ANGUS M.
 APPLICANT: MERCHANT, KEVIN J.
 TITLE OF INVENTION: INHIBITORS OF PHOSPHOINOSITIDE-SPECIFIC
 TITLE OF INVENTION: PHOSPHOLIPASE C
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSES: DAVID A. MUTHARD
 STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
 CITY: RAHWAY
 STATE: NEW JERSEY
 COUNTRY: U.S.A.
 ZIP: 07065

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/138,133
 FILING DATE:
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: MUTHARD, DAVID A.
 REGISTRATION NUMBER: 35,297
 REFERENCE/DOCKET NUMBER: 18938
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (908) 594-3903
 TELEFAX: (908) 594-4720
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1290 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-138-133-2

78 NSDLSKEAFKYLMPDNLGVHNVVHODMTQPMHSHYFTFTGHSNLTGNSLSDSDTP 137
 303 ---FSKE-----NSVNSQLDVCAPETMNNPLSHYWISSSHNTYLTGDFSSSESSLEA 352
 138 IAAALRRGVVVELDLWPDGKGMKVTGNTLTNPVSFKCVTAIKNNAFFTSXPVCVT 197
 353 YARCLRMGRCIELDCWDGPMPIYHGHLLTKIKESDVLHTIKHAFVASEYPVLS 412
 198 IEDHLTSELQHAAILQILGDLALYPTTDLALVEFPSPESLKRKLIISTK----- 249
 413 IEDHCSIAQORNAQHFRKVLGDTLLTKPVDIAADGLSPNQLKRLIKHKKLAEGSAY 472
 250 -----SOKEMSTP----- 249
 473 EEVPTSMYSENDISNKGILYLEDVNVHWPVHYFVLITSSKIYSEETSSDOGNEDE 532
 250 -PKPE---YLEACSTOK-----LAMENRNLEVEEKEKLE-----OTTAPLEENHIL 294
 533 EEPKASGSELHSSSEKWFHGLGAGDRGRHIAERLLTEYCIETGAPDGSFLVRESETFV 592
 295 GENTPSLRKEVEVL-----SOKEMSTP----- 316
 593 GDYTLSEWRNGKQVHCRIHSRQDAGTPKFFLTDNLVFDLSLYLTHYQVPLRCNEFEMR 652
 317 -----AELNSRSPDLGEATSTR-----YKSNKNDGND----- 343
 653 LSEVPQTNHAKESKETHASLTRAQAEHMLMRVPRDGAFLVRKRNEPNSYSAISFRAEGKI 712
 344 -----NPKHE----- 348
 713 KRCRVQEGQVVMGNSEFDSLDLSYVEKHPYKMKLRYPINEEALEKIGTAEPDYG 772
 344 -----NPKHE----- 348
 773 ALYEGRNPGFVEANPMTFKCAVKALFDYKAQREDELFTKSAIQNVKODGGWGRGD 832
 349 -----KYA 351
 833 YGKKQLMFPNSVVEEMINPAILEPEREHLIDENSPLGLDLRGVLDVPACQIAIRPEGKNN 892
 352 RLITIRL-----AKHAKGTSMEHR-----LO 372
 893 RLFEVSIEMPSVAQSLDVAADSOEQLDWWKIREVAQPADARLTGEGMKMERKKIALE 952
 373 VDES-----KRI-----SLSEKLEKVEKWEALVRFKTNIL-----R 408
 953 LSELVVCYCRPVFDEKIGTERACRYRMSSEPEIKAEKYNNKAKG--KFLQYNRLQLSR 1010
 409 VYPAANRVNSNFCPTLAWNYGAQVVAQNMGGYKELWQAFGKFGNGGCGYVYLKPYLL 468
 1011 IYKQRLDSSNYDPLPMWICGSQLVALNFQTPDKPMQMOALFMAAGHCGYVQLQPTWR 1070
 469 ENLPSPVNPNTSPRN--TTLILKIKVMTTLGWDAFKSRHFDLFPSPDPFTFTRVIVGVPA 527
 1071 DE--AFDPDKSLRGLPEVCICIEVGA---RHLKNGRGIVCP---FVEIEVAGAEY 1121
 528 DEAKWITS--VDNSWAPHW--NEDHEFALKCPCLALLRTEVRDHDHDSKDFEGQCLPIH 585
 1122 DSTQKTEFVDNLGPNVPKAPFHFQISNPEFAPLFRVYVEEDMFSDONFLAQAATFPVK 1181
 586 EVRDGYRCMOM 596
 1182 GLKGTGYRAVPL 1192

RESULT 2
 US-08-138-133-2
 ; Sequence 2, Application US/08138133
 ; Patent No. 5519163
 ; GENERAL INFORMATION:
 ; APPLICANT: GIBBS, JACKSON B.
 ; APPLICANT: KOBLAN, KENNETH S.

Query Match 12.3%; Score 409.5; DB 1; Length 1290;
 Best Local Similarity 20.0%; Pred. No. 5.6e-27;
 Matches 194; Conservative 88; Mismatches 252; Indels 437; Gaps 26;

QY 22 GEVFTIYSNERMSA-EGLLKFLHTEQGDV---FTLDDAKQIMERIRKDKKSFGLASI 77
 Db 263 GELWAY---DLQVQEFMLSEFLRDLREIEEPYFFDELVTFL----- 302
 QY 78 NSDLSKEAFKYLMPDNLGVHNVVHODMTQPMHSHYFTFTGHSNLTGNSLSDSDTP 137
 Db 303 ---FSKE-----NSVNSQLDVCAPETMNNPLSHYWISSSHNTYLTGDFSSSESSLEA 352
 QY 138 IAAALRRGVVVELDLWPDGKGMKVTGNTLTNPVSFKCVTAIKNNAFFTSXPVCVT 197
 Db 353 YARCLRMGRCIELDCWDGPMPIYHGHLLTKIKESDVLHTIKHAFVASEYPVLS 412
 QY 198 IEDHLTSELQHAAILQILGDLALYPTTDLALVEFPSPESLKRKLIISTK----- 249
 Db 413 IEDHCSIAQORNAQHFRKVLGDTLLTKPVDIAADGLSPNQLKRLIKHKKLAEGSAY 472
 QY 250 -----SOKEMSTP----- 249
 Db 473 EEVPTSMYSENDISNKGILYLEDVNVHWPVHYFVLITSSKIYSEETSSDOGNEDE 532
 QY 250 -PKPE---YLEACSTOK-----LAMENRNLEVEEKEKLE-----OTTAPLEENHIL 294
 Db 533 EEPKASGSELHSSSEKWFHGLGAGDRGRHIAERLLTEYCIETGAPDGSFLVRESETFV 592
 QY 295 GENTPSLRKEVEVL-----SOKEMSTP----- 316
 Db 593 GDYTLSEWRNGKQVHCRIHSRQDAGTPKFFLTDNLVFDLSLYLTHYQVPLRCNEFEMR 652
 QY 317 -----AELNSRSPDLGEATSTR-----YKSNKNDGND----- 343
 Db 653 LSEVPQTNHAKESKETHASLTRAQAEHMLMRVPRDGAFLVRKRNEPNSYSAISFRAEGKI 712

QY 344 ----- 343
Db 713 KHCVRQEGQTVMLGNSEFSLVDLSIYERKPLRYKMKLRYPINEEALEKIGTAEPDYG 772
QY 344 -----NPKHF----- 348
Db 773 ALYEGRNPFGYVEANPMTFFKCAVKALFDYKAQREDELFTFKSAIONVEKODGQWWRGD 832
QY 349 -----KVA 351
Db 833 YGKKQLPFPNYSVEEMINPAILEPEREHLDENSPLGLRLGVLDVPACQAIAPRGN 892
QY 352 RLITIRL-----AKHAGTSMHR-----LQ 372
Db 893 RLFFVESISMPVAQNSLDVAADQELQDWKKIREVAQTADARLITECKMMERRKKIALE 952
QY 373 VDESV-----KRI-----SLESKEKVKVWPALVKFKNKL-----R 408
Db 953 LSELVYCRPVDFDEKIGITERACRYRDMSSFPETRAEYVNAKAGK--KFLQYNRLQLSR 1010
QY 409 VYPAANRVNSSFPCPTLAWNYGAOMVONMOGYGKELQWAFKPKNGCGCYVLKPOYLL 468
Db 1011 ITPKGRDSSNYDPLPMWICSGJVALNFQPDKPMQNALFMAGHCGYVLOPSTMR 1070
QY 469 ENLPSGVFPNTPSPRN--TTLILKIKVMTTLGWDAFSAKRRHFDLFSPPDFFTRVIVGVPA 527
Db 1071 DE--AFDPDKSLRGLRGLPCVICIEVGA---RHLPKNGRGI VCP---FVEIEVAGAEY 1121
QY 528 DEAKWKT--VVDNSWAPIW--NEDHEFAKCPDELALLRTEVRDHDHDDSKDEFEGOTCLPIH 585
Db 1122 DSTKOTFEVVDNGLNVMPAKPFHQISNPEFAPLREVVEEDMFSDQNLQAOTEPVK 1181
QY 586 EVRDGVCRCMQM 596
Db 1182 GUKTGIRAVPL 1192

RESULT 3

US-08-235-836C-112
; Sequence 112, Application US/08235836C
; Patent No. 6248562
; GENERAL INFORMATION:
; APPLICANT: Dunn, John J.
; APPLICANT: Luft, Benjamin J.
; TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising
; TITLE OF INVENTION: Borrelia Polypeptides and Uses Therefor
; NUMBER OF SEQUENCES: 144
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brookhaven National Laboratory
; STREET:
; CITY: Upton
; STATE: NY
; COUNTRY: USA
; ZIP: 11973
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/235,836C
; FILING DATE: 29-APR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,191
; FILING DATE: 01-11-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Bogosian, Margaret C.
; REGISTRATION NUMBER: 25,324
; REFERENCE/DOCKET NUMBER: BNL93-28A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 282-7338

; TELEFAX: (516) 282-3729
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 573 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-235-836C-112

Query Match 3.7%; Score 123.5; DB 4; Length 573;
Best Local Similarity 17.5%; Pred. No. 0.022;
Matches 85; Conservative 84; Mismatches 209; Indels 109; Gaps 15;

QY 15 DPEODLGEV--FTIYSENERMSAEGLLKFLHTEOGDVFDTLDD----- 56
Db 32 DGKVDLTIATVDKLELKTSDKNNNGSVLEGVKADKSKVKLTISDDLGOTTLEVFKEGDKT 91
QY 57 --AKQIMERIRKDWKKSF-----GLASINSDLSKEAFRKYLMN 92
Db 92 LVSKKVTSKDKSSSTEERKEKEGVSEKIIITRADGTRLEYTGIKSDGSKAKAEVLKGVYLE 151
QY 93 PDLNGVLHVHQDMTQPMSHYFIFTGHNLYLTGNQLSSDSDPTIAAALRRGVRVVELD 152
Db 152 GTLTAERTTLVKBGTVTLSKNISKSG-----EVSVELNDTSSAATKTA----- 197
QY 153 LWPDDKGMKMTGNTLTNPVSFKCVTAIKNNAFTSEV-----PVCVTIEDHL 202
Db 198 AWNSGTSTLITVNSKTKDLV-----TKENTIVQQYDSNGTKLEGSVAEITKLEI 251
QY 203 TSELQGHAAETLEQIL-----GDALYYPPTTDALVFPPSPESLKRKIIISTKPKR 252
Db 252 KNALKGHPMD--EKLKSKDKKASKDKGKALDLDRELNSKASSEKSKAKEEETTKGSKQ 309
QY 253 EYLEACSTQKLAMENRLVEELEKEDKLEQTTTAPLEE-----NHILGENTPSLR 302
Db 310 SLGLNNDENLMPEDQKLEPKVKLDSKKE--FKPVSEVEKLDKIFKSNNNVGLSPLDK 367
QY 303 KEVELSQEMSTPAELN--SRSPDLGEATSTRYKSDGNDGNPKHF-----KYARLI 354
Db 368 SSYKDISKEETVKNQVNLQKTRPOVKDQVTSINEDLTMSIDSSSPVLEVIDPTNGLG 427
QY 355 TIRLAKHAKGTSMEHRLQVDVSKRISLSLESKLEKVVKEWPEALVFTOKNIRLVYPAAN 414
Db 428 TLQIDLNTGVLKKESTQ--QGIRQYGIYERKDLVVKMDSGKAKL---QILDKLENLK 482
QY 415 RVNSNF 421
Db 483 VVSESNF 489

RESULT 4

US-08-328-254-6
; Sequence 6, Application US/08328254
; Patent No. 5710022
; GENERAL INFORMATION:
; APPLICANT: Zhu, Xueliang
; APPLICANT: Lee, Wen-Hwa
; TITLE OF INVENTION: A No. 5710022el Nuclear Mitotic Phosphoprotein
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/328,254
;; FILING DATE: 24-OCT-1994
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/141,239
;; FILING DATE: 22-OCT-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Campbell, Cathryn A.
;; REGISTRATION NUMBER: 31,815
;; REFERENCE/DOCKET NUMBER: P-CJ 1191
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (619) 535-9001
;; TELEFAX: (619) 535-8949
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 2482 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-328-254-6

Query Match 3.6%; Score 120; DB 1; Length 2482;
Best Local Similarity 21.4%; Pred. No. 0.46;
Matches 129; Conservative 79; Mismatches 216; Indels 178; Gaps 31;

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QY 37 EGLLKFLHTEQGDVFTLDDAKQIMERIRKDWKKSFGLASINSDLSKEAFKRYLMNPDLN 96
Db 104 EHKQLLSNEIMDKRCYQDLHAEYSLR-----DLLKSKDASLVNED-- 147
QY 97 GVLHNVVHQ-----DWTQPMSHYFIFTGHNSYLTGNLSLSDSDTPIAAALRRGVRVVE 150
Db 148 -----HQSLLAFDQOPAMHHSF-----ANIIEGQSMPS-----ERSECRLE 185
QY 151 LDLPDDKGGMKVTHGNTLTNPVSFKCVTAIKNNAFTSEYPCVVTIEDHLTSELQCHA 210
Db 186 ADQSPKN-----SAILQNRVDSLEF--SLESQKQMSDLQKQC 221
QY 211 AEILQILGDALYPPPTDALVE--FPSPELKRKIIIST--KPPKEYLEACSTOKLAME 266
Db 222 EELV-QIKGE-----IEENLMKAEQMHQSFAETSQRISKLEQEDTSAHONVVAE 269
QY 267 NRNLVEELEKE-----DKLEQTTFAPLEE-----NHILGENTPSPSRKEVEVLS--QKEMST 315
Db 270 TSLALENKEKELQLLNDKVE--TEQAEIQELKKSNNHLLSDLSKELQSLSETLSLEKKEMSS 328
QY 316 PAELNSRSPDLGEATSTRYSKNDGNDNPKHFKYARLITIRLAKHAKGTSMEHRLQVDE 375
Db 329 IISLNKREIBELTQENG--LKEINASLNQEKMNLIQ-----KSESFAN--YIDE 374
QY 376 SVKRIS-LSFS-KLEVV-----EKWPEALVKFTOKNLRVYPAANRVNS-----NFCP 423
Db 375 REKISLSQYQKELQLLQRCETEGNAYEDLSQK-----YKAAQEKSKLECLINECT 429
QY 424 TLAWNYGAOMVAONMOGYKELMQAFK-----FKNGGCGYVLKPYQLLENLPS 473
Db 430 SL-----CENRKNLEQLKEAKAKEHQEPLTKLAFABERNQNLMELETVQQAIRS 480
QY 474 GVPFNTPSPRNTLILKIKVMTLGDWDAFSAKRHFDLFPDPDFTRVIVGVPADEAKWK 533
Db 481 EMTDNQNSKSEAGGLKQELMTLKEQNKMKQEVNDLQLENEQLMKVM-----K 529
QY 534 TSVDVNSWAPHNWEDHEFALKCPAL--LRIEVRDHD--SKDFEGOTCLPIHEVR-D 589
Db 530 TK-----HE-----CNLESEPIRNSVKERESERNQCNKQMDLEVKEISLD 572
QY 590 GY 591
Db 573 SY 574
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RESULT 5
US-08-353-700-1

;; Sequence 1, Application US/08353700
;; Patent No. 5599919
;; GENERAL INFORMATION:
;; APPLICANT: YEN, TIMOTHY J.
;; APPLICANT: RATTNER, JEROME B.
;; TITLE OF INVENTION: NUCLEIC ACID ENCODING A
;; TITLE OF INVENTION: TRANSIENTLY-EXPRESSED KINETOCHORE PROTEIN,
;; TITLE OF INVENTION: AND METHODS OF USE
;; NUMBER OF SEQUENCES: 4
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: DANN, DORFMAN, HERRELL AND SKILLMAN
;; STREET: 1601 MARKET STREET, SUITE 720
;; CITY: PHILADELPHIA
;; STATE: PA
;; COUNTRY: USA
;; ZIP: 19103-2307
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/353,700
;; FILING DATE: 09-DEC-1994
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: REED, JANET E.
;; REGISTRATION NUMBER: 36,252
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (215) 563-4100
;; TELEFAX: (215) 503-4044
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 3248 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; ORIGINAL SOURCE:
;; ORGANISM: HUMAN
US-08-353-700-1

Query Match 3.6%; Score 120; DB 1; Length 3248;

Best Local Similarity 21.4%; Pred. No. 0.71;
Matches 129; Conservative 79; Mismatches 216; Indels 178; Gaps 31;

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QY 37 EGLLKFLHTEQGDVFTLDDAKQIMERIRKDWKKSFGLASINSDLSKEAFKRYLMNPDLN 96
Db 736 EHKQLLSNEIMDKRCYQDLHAEYSLR-----DLLKSKDASLVNED-- 779
QY 97 GVLHNVVHQ-----DWTQPMSHYFIFTGHNSYLTGNLSLSDSDTPIAAALRRGVRVVE 150
Db 780 -----HQSLLAFDQOPAMHHSF-----ANIIEGQSMPS-----ERSECRLE 817
QY 151 LDLPDDKGGMKVTHGNTLTNPVSFKCVTAIKNNAFTSEYPCVVTIEDHLTSELQCHA 210
Db 818 ADQSPKN-----SAILQNRVDSLEF--SLESQKQMSDLQKQC 853
QY 211 AEILQILGDALYPPPTDALVE--FPSPELKRKIIIST--KPPKEYLEACSTOKLAME 266
Db 854 EELV-QIKGE-----IEENLMKAEQMHQSFAETSQRISKLEQEDTSAHONVVAE 901
QY 267 NRNLVEELEKE-----DKLEQTTFAPLEE-----NHILGENTPSPSRKEVEVLS--QKEMST 315
Db 902 TSLALENKEKELQLLNDKVE--TEQAEIQELKKSNNHLLSDLSKELQSLSETLSLEKKEMSS 960
QY 316 PAELNSRSPDLGEATSTRYSKNDGNDNPKHFKYARLITIRLAKHAKGTSMEHRLQVDE 375
Db 961 IISLNKREIBELTQENG--LKEINASLNQEKMNLIQ-----KSESFAN--YIDE 1006
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us-09-828-447-12.rai

Sun Jul 28 10:34:35 2002

376 SVKRIS-LSKS-KLEKVV-----EKWPEALVKTOKNIRLVYPAANRVNS--NFCP 423
1113 EMTDNQNSKSEAGGLKQEIIMTLAEQNMOKNEVDNLOEQLMKVM-----K 1161
424 TLAWNYGAQWVAQNMQYKELWQAFK-----FKNGGCGYVLKPYLLENLPS 473
1007 REKSISELSDOYKQEKLLILQRCETGNAYEDLSQK-----YKAAQEKNSKLECLINECT 1061
424 TLAWNYGAQWVAQNMQYKELWQAFK-----FKNGGCGYVLKPYLLENLPS 473
1062 SL-----CENRKNELQLEAKFAKEHOFETKLAFAERNQNMLELETVOQALRS 1112
474 GVPFNTPSPRNTLLIKTKVMTLWMDKAFSKRHFDFSPDPFTRVIVGVPADEAKWK 533
1113 EMTDNQNSKSEAGGLKQEIIMTLAEQNMOKNEVDNLOEQLMKVM-----K 1161
534 TSVDNSWAPHNWEDHEFAKCPAL--LRIVRDHDD--SKDFEGOTCLPIHEVR-D 589
1162 TK-----HE-----CONLESEPIRNSVKERESERNOCNFKPQMDLEVKELSLD 1204
590 GY 591
1205 SY 1206

RESULT 6
PCT-US95-16216-1
Sequence 1, Application PC/TUS9516216
GENERAL INFORMATION: Timothy J.
APPLICANT: Ven, Timothy J.
APPLICANT: Ratner, Nucleic Acid Encoding a Transiently
TITLE OF INVENTION: Expressed Kinetochores Protein, and Methods of Use
TITLE OF INVENTION: 4
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS: Dana, Dorfman, Herrell and Skillman
ADDRESS: 1601 Market Street Suite 720
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16216
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA: US 08/353,700
APPLICATION NUMBER: 09-DEC-1995
FILING DATE: 09-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3248 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE:
PCT-US95-16216-1

Query Match 3.6%; Score 120; DB 5; Length 3248;
Best Local Similarity 21.4%; Pred No. 0.71; Indels 178; Gaps 31;
Matches 129; Conservative

736 EHKQLLSNEIMDKRCYQDLHAEYSLR-----DLLKSKDASLTNED-- 779
97 GVLNVVHO-----DMTPMSHYFIFTGHNLYLGNQLSSDSTPIAALARGVRYVE 150
780 -----HORSLLAFDOOPAMHHSF-----ANLIGECSMPS-----ERSECRLE 817
151 LDLPDDKGGKMKVTHGNTLTNPVSTOKVTAIKNNAPFTSEYPCVVTIEDHLSLQGH 210
818 ADQSPKN-----SAILQNRVDSLEF-----SLESOKOMNSDLOKQC 853
211 AEILEQIGDALIYPPPTDALVE--FPSSESLKRIIIST--KPPKYLEACSTOKLAME 266
854 EELV-QIKE-----IEENLMKAEOMHQSFAVETSQRIKQEDTSAHQNVAE 901
267 NRNLVELEKE-----DKLEOTTTFAPLEE-----NHILGENTPSLKEVEVLS--QKEMST 315
902 TSLALENKEKELQALLNDKVE--TEQAEIOELKSKNHLSDLSLQELLSLSEKKEKMS 960
316 PRLNRSRPSDLGATSTRYSKNSDNDONPHFYKARLITIRLAKHAKTSMHRLOVDE 375
961 IISLANKREIEELTOENGT--LKEINASLNOEKNLIQ-----KSEFAN--YIDE 1006
376 SVKRIS-LSKS-KLEKVV-----EKWPEALVKTOKNIRLVYPAANRVNS--NFCP 423
1007 REKSISELSDOYKQEKLLILQRCETGNAYEDLSQK-----YKAAQEKNSKLECLINECT 1061
424 TLAWNYGAQWVAQNMQYKELWQAFK-----FKNGGCGYVLKPYLLENLPS 473
1062 SL-----CENRKNELQLEAKFAKEHOFETKLAFAERNQNMLELETVOQALRS 1112
474 GVPFNTPSPRNTLLIKTKVMTLWMDKAFSKRHFDFSPDPFTRVIVGVPADEAKWK 533
1113 EMTDNQNSKSEAGGLKQEIIMTLAEQNMOKNEVDNLOEQLMKVM-----K 1161
534 TSVDNSWAPHNWEDHEFAKCPAL--LRIVRDHDD--SKDFEGOTCLPIHEVR-D 589
1162 TK-----HE-----CONLESEPIRNSVKERESERNOCNFKPQMDLEVKELSLD 1204
590 GY 591
1205 SY 1206

RESULT 7 484-2
US-09-198-484-2 Application US/09198484
Sequence 2, 6162435
GENERAL INFORMATION:
APPLICANT: Minion, F. Chris
APPLICANT: Hsu, Tsungda
TITLE OF INVENTION: RECOMBINANT MYCOPLASMA HYOPNEUMONIAE VACCINE
FILE REFERENCE: 19000.028/P028
CURRENT APPLICATION NUMBER: US/09/198,484
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 2
LENGTH: 904
TYPE: PRT
ORGANISM: Mycoplasma hyopneumoniae
US-09-198-484-2

Query Match 3.5%; Score 115; DB 4; Length 904;
Best Local Similarity 20.1%; Pred. No. 0.26; Indels 148; Gaps 22;
Matches 104; Conservative 73; Mismatches 192;
ASINSDLSKEAFK 88
51 DFTLD---DAKOIMERIRKDWKSKFGL-----ASINSDLSKEAFK 88
234 DYQLDPVLDKRLKLLTLNKLKDKGLVGLNLVQISTKTKTNLNLVLRGAISNQLSK--ILK 291
89 YLMPDLNGVLHNVVHDMTQ-----PMASHYFTFTGHSNLYLTGOLSS-----DSS 134

us-09-828-447-12.rai

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Db 292 SWLETNJGKLTCKDDLOWALVKDKISLSYW-YGSPNSKVNTSOILTKSKFKDFDLS 350
Qy 135 DTPAAALRRGVRVVELDMPD-DKGGMKVTHGNTLNPVSKVCVTA-IKNA-----F 187
Db 351 ENF--FLNTKIGTVYLSIIPKLLDPSQISVDKKLVENOKIRFEITASLAKRAIDKKE 408
Qy 188 FTSEYPCVCTI-----EHLTSELOGHAAEILEQILGD 220
Db 409 IIQDLPVFDLKVDFNKYQAAVQMGFTIKAVREFSNPEDODAKTLSSN--EIKQV--D 464
Qy 221 ALYVPPTDALVEFPSPSLARKIIISTKPPREYLEACSTOKLAWENNRNVEELEKEDKL 280
Db 465 RLEFELAKTVTNLENPSEVLKSYLLNT---GKYLVDODQKQKQELKTVIEGLSKANT 521
Qy 281 EOT-----TFAPLENHILGENTPFLRKEVLSOKEMSTPAELNRSRSD 327
Db 522 OKTEKNSPTOKKPEVSLAKTTSNTAKTVKYSTFAEAKGQSQSQOTOPVSTSPQSON 581
Qy 328 GEATSTRYSKSDNDGNPKH-----FKYARLITIRLAKHAKGTSMEHRLVDVSKRI 380
Db 582 SLPNST--SSNSVLENEKFTGTSIWTAFNANI-----YNLENTKSEYEI 624
Qy 381 SLSEKSL--EKVKEKPEALVKFTQKNILRYVPAANKVNSNFCPTLAWNYGAQVQV- 436
Db 625 STIGNKLFDFKLVKDNQNLILAOSKISLN-----NIINSKSAVDIIRKFNPDVLDG 679
Qy 437 --NMGGYKELWQAFKFGKNGGCGYVLPQYILENL 471
Db 680 TYNQNGKD-----KAEFILKDL 698

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RESULT 8

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US-07-977-434-8
; Sequence 8, Application US/07977434
; Patent No. 5466591
; GENERAL INFORMATION:
; APPLICANT: Gelfand, David H.
; TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Wordperfect 7
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07977434
; FILING DATE: 28-SEP-1990
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 590,490
; FILING DATE: 28-SEP-1990
; APPLICATION DATA:
; FILING DATE: 28-SEP-1990
; APPLICATION NUMBER: US 590,213
; FILING DATE: 28-SEP-1990
; APPLICATION DATA:
; FILING DATE: 15-MAY-1990
; APPLICATION NUMBER: US 523,394
; FILING DATE: 12-JAN-1988
; APPLICATION DATA:
; APPLICATION NUMBER: US 063,509

```

Query Match

```

Best Local Similarity 3.4%; Score 113.5; DB 1; Length 834;
Matches 114; Conservative 87; Mismatches 195; Indels 221; Gaps 29;
Qy 14 GDPEODL-----VGEVFTYSENERMSAEGLLKFLHTEQGVDFDIDAK--QIMERIR- 65
Db 188 GDPSDNLPGVKGIGERTALKLLKKGWSLENILK-----NLDVVKPESVREIKA 236
Qy 66 --KDWKSFGLASINSL-----SKEAFKYLMPDNLGVHNVHVDMDTOPM 111
Db 237 HLEDLKLSELSRVHSDLPLEVDFAFRREPREDGRLAFLEKLEFGSLHHEFGLLEAPL 296
Qy 112 SHYFTTGHNSYLTGNLSSDSDTPIAAALRRGVVVELDLPDDKGGMKVTHGNTLTN 171
Db 297 -----EEAP-----WPPPECAFV---GFVLSR 315
Qy 172 PVSF--OKCVTAIKNNAFTSEYPCVCTIEDHLTSELOGHAAEILEQI-LGDALYYPPT 227
Db 316 PEPMAELKALAAKEGVRHRAKDPL-AGLD--LKEVRGLAKDLAVLALREGDLAPS 372
Qy 228 TDALV-----EFPSPESLKRKIIISTKPPREYLEACSTOKLAME--NRNVEELEKED 278
Db 373 DDPMLLAYLLDPSNTTPEGVARRY-----GGEWTEDAAHALLAERLOONLLERLKEE 426
Qy 279 KL-----EOTTFAPLEENH-----LGENTPSLRKEVEVLSOKEMST 315
Db 427 KLLWLYOEVEKPLSRVLAHMEATGVRDLVDVAYLAKLSLELAISEIRLEEVEFRLA---CH 482
Qy 316 PAELNRSRPSD-----LGEATSTRYSKSDNDGNPKHFKYARLITIRLAKHAKG 364
Db 483 PFNLNRSQLEVRVLFDELRLPALGKTQKT--CKRSTSAVLEALREAHPIVEKILQHREL 540
Qy 365 TSWEH-----RL-----QVDESVAKISLESKLEKVEK----- 393
Db 541 TKLNNTYVDPLPGVHPRTGRHLTRFNOTATGRUSSDPNLPNIPTIRPLOORIRRAF 600

```


GENERAL INFORMATION:
APPLICANT: Gelfand, David H.
TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF
THERMOSTABLE DNA POLYMERASES
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cetus Corporation
STREET: 1400 Fifty-third Street
CITY: Emeryville
STATE: California
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
FILING DATE: 19910930
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 590,490
FILING DATE: 28-SEP-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 590,466
FILING DATE: 28-SEP-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 590,213
FILING DATE: 28-SEP-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 523,394
FILING DATE: 15-MAY-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 143,441
FILING DATE: 12-JAN-1988
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 063,509
FILING DATE: 17-JUN-1987
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 899,241
FILING DATE: 22-AUG-1986
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 746,121
FILING DATE: 15-AUG-1991
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US90/07641
FILING DATE: 21-DEC-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 585,471
FILING DATE: 20-SEP-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 455,611
FILING DATE: 22-DEC-1989
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 609,157
FILING DATE: 02-NOV-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 557,517
FILING DATE: 24-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Sias Ph.D., Stacey R.
REGISTRATION NUMBER: 32,630
REFERENCE/DOCKET NUMBER: Case No. 2580
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-420-3300
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 834 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US91-07035-8

Query Match 3.4%; Score 113.5; DB 5; Length 834;
Best Local Similarity 18.5%; Pred. No. 0.3;
Matches 114; Conservative 87; Mismatches 195; Indels 221; Gaps 29;
QY 14 GDEQDL-----VGEVFTIYSENERMSAEGLLKFLHTEQGDVDTLDDAK--QIMERIR- 65
Db 188 GDSNLPVKGIGETALKLLKEWGSLENIK-----NLDVRKPVSRRIKA 236
QY 66 --KDWKKSFGLASINSDL-----SKEAFKRYLNNPDLNGLVHNVHODMTQPM 111
Db 237 HLEDKLSLELSRVSDLPLEVDFAARRREPDRGLRAFLERLEFGSLHFEGLLEAPPL 296
QY 112 SHYFIFTGHSYLTGNQLSSDSTPIAAALRRGVVRVVDLWDDPKGGMKVTHGNTLTN 171
Db 297 -----EBAP-----WPPGGAFFV---GFVLSR 315
QY 172 PVSF---QKCVTAIKNNAFFTSEYPCVVTIEDHLTSELQGHAAEILBOI--LGDALYYPPT 227
Db 316 PEPMAELKALACKEGRVHRAKDPL--AGLKD--LKEVRGLLAKDLAVLALREGLDLAPS 372
QY 228 TDALV-----EPPSPESLKRKIIISTKPPKEYLEACSTQKLAME--NRNLVEELEKED 278
Db 373 DDPMLLAYLLDPSTNTPEGVARRY-----GGWETDAAHRALLAERLQQLNLERLKGE 426
QY 279 KL-----EQTFAPLEENHI-----LGENTPSLRKEVEVLSQKEMST 315
Db 427 KLLWLYQVEVEKPLSRVLAHMEATGVRDVAIYKALSLELAEEIRLEEEVFRLA----GH 482
QY 316 PAELNSRSPSD-----LGEATSTRYSKSDNGNDNPKHKYVARLITIRLAKHAG 364
Db 483 PFNLNSRDQLERVLFDLRLPALGKTQKT--GKRSTSAALVLEALRAHPIVEKILQREL 540
QY 365 TSMEH-----RL-----QVDESVKRISLSESKLEKVVEX----- 393
Db 541 TKLNTYVDPPLGVLVHPRTGRHLTREFNQATATGRLLSSDPNLQNPITPQIRRAF 600
QY 394 ----WPEALVKFTQ-----KNILRVYPAANRVNSNFCPTLAWNYGA--QMV 434
Db 601 VAEGWALVALDYQIELRVLAHLSDENLIRVFQEGKDIHQ-----TASWFGVSPEAV 656
QY 435 AQNMGGYKELWQAFKFGKNGCGYVLAPQYLLLENLPSPGVFPNPTSPRNTTILKIKVM 494
Db 657 DPLMRAAKTV-----NFGVLYGMSAHLRSQEL--AIPVEEA----- 691
QY 495 TTLGWDKAFSKRHEDLF 511
Db 692 -----VAFIERYQSF 702
RESULT 11
US-09-026-343-2
; Sequence 2, Application US/09026343
; Patent No. 6008018
; GENERAL INFORMATION:
; APPLICANT: DUAN, D. ROXANNE
; APPLICANT: SHILATIFARD, ALI
; APPLICANT: CONAWAY, JOAN W.
; APPLICANT: CONAWAY, RONALD C.
; TITLE OF INVENTION: ELL2, A New Member of an ELL Family of
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION: PatentIn Release #1.0, Version #1.30
 APPLICATION NUMBER: 19-FEB-1997
 FILING DATE: US/09/026,343
 CLASSIFICATION: Herewith
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/038,447
 FILING DATE: 19-FEB-1997
 NAME: GOLDSTEIN, JORGE A.
 REGISTRATION NUMBER: 29,021
 REFERENCE/DOCKET NUMBER: 1488-0880001
 TELEPHONE: (202) 371-2600
 TELEFAX: (202) 372-2540
 INFORMATION FOR SEQ ID NO: 2:
 LENGTH: 640 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-026-343-2

Query Match
 Best Local Similarity 3.24; Score 107; DB 3; Length 640;
 Matches 91; Conservative 73; Mismatches 151; Indels 174; Gaps 24;
 QY 9 SCTPKGDEODLVEFTI--YSENE---RMSAEG-----LLKFLHTEQGDVD 51
 Db 198 SSTISORPYRDRVHLLALKAYKPELLARLOKQDGVNOKDKNSLGAIIQQVANLSKDL 257
 QY 52 FTLDLDAQWIERIKDKW--KSEGLASINSISKEAFKRYLWNPDLNGLVHNVVHDMQ 109
 Db 258 YTLKD--YVEKLRQDWPYSEIDRSLSVLSRK-----LNFSONA----- 297
 QY 110 PMSHYFITGHSNLTGNLSSD---SDTPIAALRRGVVVELDLPDDKGGKMYTHG 166
 Db 298 -----TGTSRSRSPVCSRDVSSPOKRLDSEFDPLMNKA--RISH- 339
 QY 167 NLTNPVPSQKCVTAIKNAFFTEYPCVVTIEDHLTSELQHAEEILQILDALYYP 226
 Db 340 ---LTVNP-----PTLNGHLNPTSEKSA-----GLPLPP 367
 QY 227 TTDALVEPSPESLKRKIISKPKP-----EYLEACSTQKIAM---ENRNVEE 273
 Db 368 AAMAI---PTPLPSTYLPISHPPOIVNSNSPSTPGRTQDLPVDSFSQNDIYE- 423
 QY 274 LEKEDLEQTF-----APLEENHILG-----ENTPSLRKEVEV 307
 Db 424 -DQDKYTSRTSLETLPQSVLLKCPKPMENHSHKSKKSKKHKKDKQIKKHDIET 482
 QY 308 LSOKEMSTP-----AELNSRSPDLG-----EATST-----RYSKSN 339
 Db 483 IEKEEDLKREEIAKLNSSPSSGGVKEDCTASMEPSAIELPDYLYKIYIYVSEORQ 542
 QY 340 DQND--NPKHKYARLITRLAKHAKTSMEHR-LOVDESVKRISLESKLEKVEKWE 396
 Db 543 NYKDDFNABYDEYAL-----HARMETVARFRKLDQKRLSPGSKYQNVHEVLQ 595
 QY 397 ALVKTQKN 405
 Db 596 EYQIKQSS 604

RESULT 12
 US-07-977-434-10
 ; Sequence 10, Application US/07977434
 ; Patent No. 5466591
 ; GENERAL INFORMATION:
 ; APPLICANT: Gelfand, David H.
 ; APPLICANT: Abramson, Richard D.

TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF
 NUMBER OF SEQUENCES: 38
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Hoffmann-La Roche Inc.
 STREET: 340 Kingsland Street
 CITY: Nutley
 STATE: New Jersey
 ZIP: 07110-1199
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Macintosh
 OPERATING SYSTEM: 7
 SOFTWARE: Wordperfect 2.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/977,434
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 590,490
 FILING DATE: 28-SEP-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 590,466
 FILING DATE: 28-SEP-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 590,213
 FILING DATE: 28-SEP-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 523,394
 FILING DATE: 15-MAY-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 143,441
 FILING DATE: 12-JAN-1988
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 063,509
 FILING DATE: 17-JUN-1987
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 899,241
 FILING DATE: 22-AUG-1986
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 746,121
 FILING DATE: 15-AUG-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/US90/07641
 FILING DATE: 21-DEC-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 585,471
 FILING DATE: 20-SEP-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 455,611
 FILING DATE: 22-DEC-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 609,157
 FILING DATE: 02-NOV-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 557,517
 FILING DATE: 24-JUL-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Luann Cseri
 REGISTRATION NUMBER: 31,822
 REFERENCE/DOCKET NUMBER: Case No. 5466591 8753
 TELEPHONE: (510) 814-2972
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 834 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-07-977-434-10

Query Match

3.18; Score 104.5; DB 1; Length 834;

us-09-828-447-12.rai

Sun Jul 28 10:34:35 2002

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FILING DATE: 04-JUN-1993
CLASSIFICATION: 536
PRIORITY APPLICATION DATA: US 07/986,330
PRIORITY APPLICATION NUMBER: 92
PRIORITY APPLICATION DATE: 07-DMATION:
ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Peter G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: FORS-00613
TELEPHONE: 415/703-8338
TELEFAX: 415/397-8338
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 834 amino acids
TYPE: amino acid
STRAND: linear
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-073-384C-6
3.1% Score 104.5; DB 1; Length 834;
Query Match Similarity 18.5%; Pred. No. 1.9; Indels 229; Gaps 30;
Best Local Similarity 86; Mismatches
Matches 115; Conservative
14 GDEPDL-----VGEVFTYSENERMSAGLLKFLHTEQGDVDFLDDAK--QIMERIR- 65
188 GDSNLPGLGVKGIGETKALKKEWGSLENLK-----NLDVRKPVNVEKKA 236
66 ---KMKKSGFGLASINDL-----SKAFKRYLMNPDNGVLHNVVHODTQPM 111
237 HLEDRLSLSLSRVTDLPLEVDLAQGPREGRLAFLEFGLSLLHEFGLLEAPL 296
112 SHYFTGHNSYLTGNLSSDSDTPIAAALRGVRVVDLMDPDDKGGKMGVTHGNTLTN 171
297 -----EAP-----EAP-----EAP-----EAP-----EAP----- 219
172 PVSF---QKVTAKNNAFFSEYPCVCTIEDHLSLQGHAA-----EILQILG 372
316 PEPMAELKALACRGRVHRAADPL-AGLKD--LKEVGLLAKDLAVLASREGDLVPG 274
220 DALYPTPTDALVEFSP--PSLKRKIIISTKPKPEYLEACSTOKLAME--NRNLVEEL 422
373 D---DPMALLAYLLDPSNTTPEGVARRY-----GGWTEDAAHRAHLLSERHNLKRL 480
275 EKEDKL-----QVDESVKRISLSSEKLEKVKV-----EILQILG 360
423 EGEEKLLMLYHEVEKPLSRVLAHMENTGVRLDVAILOALSLEAEIRRELEEVFRLA 536
312 EMSTPAELNSRSPD-----LGEATSTRYSKSDNDNDNPKHFKYARLITIRLAK 393
481 ---GHFENLNSRDQLERVLDELRLPALGKTOKT--GKRSTSAVLEALREAHPIVEKILQ 596
361 HAKTSMER-----RL-----QVDESVKRISLSSEKLEKVKV-----EILQILG 596
537 HRELTUKLNYVDLPVSLVHPRTGLRHTFNQATATGRSSDPLNQNIPVPTPLGQRI 431
394 -----WPEALVFTQ-----KNILRVYPAANRVNNSNFCPTLAWNYGA- 652
597 RRAFAEAGWALVALDYQELRVLAHLSGDNLRVLFQEGKDIHTQ-----TASWMEGVP 490
432 ---QWVAQNMGGYKELWQAFKFGKNGCGVILKPOYLENLPSCGVFNPTSPNTTLIK 691
653 PEAVDPLMRRAKT-----NFGVLYGMSAHLRSOEL--AIPYEEA----- 691
491 IKVMTTLGNDKAFSKRHFDLF 511
692 -----VAFIERYFQSF 702

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RESULT 14
US-08-254-359A-6

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RESULT 13
US-08-073-384C-6
Sequence 6, Application US/08073384C
Patent No. 5541311
GENERAL INFORMATION:
APPLICANT: Dahlberg, James E.
APPLICANT: Lyamichiev, Victor I.
APPLICANT: Brown, Mary Ann D.
SYNTHESIS-DEFICIENT THERMOSTABLE DNA
TITLE OF INVENTION: POLYMERASE
TITLE OF INVENTION: 29
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESS: HAVERSOCK, MEDLEN & CARROLL
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/073.384C

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us-09-828-447-12.ra1

Sun Jul 28 10:34:35 2002

; Sequence 6, Application US/08254359A

; Patent No. 5614402

; GENERAL INFORMATION:

; APPLICANT: DAHLBERG, JAMES E.

; APPLICANT: LYAMICHEV, VICTOR I.

; APPLICANT: BROW, MARY ANN D.

; TITLE OF INVENTION: 5' NUCLEASES DERIVED FROM THERMOSTABLE

; TITLE OF INVENTION: DNA POLYMERASE

; NUMBER OF SEQUENCES: 40

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: HAVERSTOCK, MEDLEN & CARROLL

; STREET: 220 MONTGOMERY STREET, SUITE 2200

; CITY: SAN FRANCISCO

; STATE: CALIFORNIA

; COUNTRY: UNITED STATES OF AMERICA

; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/254,359A

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/073,384

; FILING DATE: 06-JUN-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/986,330

; FILING DATE: 07-DEC-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: CARROLL, PETER G.

; REGISTRATION NUMBER: 32,837

; REFERENCE/DOCKET NUMBER: FORS-01000

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 705-8410

; TELEFAX: (415) 397-8338

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 834 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-254-359A-6

Query Match 3.1%; Score 104.5; DB 1; Length 834;

Best Local Similarity 18.5%; Pred. No. 1.9;

Matches 115; Conservative 86; Mismatches 191; Indels 229; Gaps 30;

QY 14 GDSQDL-----VGEFTYIYSENERMSAEGLLFLHTEGQDVDFLDDAK--QIMERIR- 65

DB 188 GDSNLPVKGIGETAKLLKMGWLENLLK-----NLDVKEPVNREKIA 236

QY 66 --KWKKSFGIASNSOL-----SKEAFKYLMPDLNGLVHNHVVHODTQPM 111

DB 237 HLEDRLSLSLRVTRDPLVDLAQRPEDREGRAFLERLEFGSLHFEGLLEAPAPL 296

QY 112 SHYFIFTGHNLSYLTGNQLSSDSTPIAALRGVRVVDLWPDGKGMKVTHGNTLTN 171

DB 297 -----EEAP-----WPPGAFV---GFVLSR 315

QY 172 PVSF---QKCVTAIKNNAFFTSYPCVVTIEDHLTSELOGHAA-----EILEQILG 219

DB 316 PEPWAEKALACRGRVHRAADPL-AGLKD--LKEVRGLLAKDLAVLASREGDLVPS 372

QY 220 DALYXPTTDALVEFPF-----PESLKRKIIISTKPKKEYLEACSTQKLAME--NRNVEEL 274

DB 373 D----DPMALLAYLLDPSNTTPEGVARY-----GGWTEDAARHALLSRLHNLKRL 422

QY 275 EKDKL-----EOTTFAPLEENHI-----LGENTPSLRKEVEVLSQK 311

Db 423 EGEKLLWLVEYKPLSRVLAHMEATGVRDVAQLQALSLAEETRRLEEEVFRLA-- 480

QY 312 EMSTPAELNSRSPD-----LGEATSTRYSKSGNDNDNPKHKFKYARLITIRLAK 360

Db 481 --GHPFNLSRDQLERVLFDLELPLALGKTQKT--GKRSTSAVLEALREAHPIVEKILQ 536

QY 361 HAKGTSMEH-----RL-----QVDESVKRISLSSEKLEKVVVEK----- 393

Db 537 HRELTKLNTYVDPLPSLVHPRTGRLTRFNQTATATGRLSSSDPNLQINIPVPTPLGQRI 596

QY 394 -----WPEALVKETQ-----KNILRVYPAANRVNSNCFPTLAWNYGA- 431

Db 597 RRAFAEAGWALVDYISQIELRLVLAHLSGDENLIRVQEGKDIHTQ-----TASNMFGVP 652

QY 432 -OMVAQNMQYCKELWQAFKFGKNGCGGYVLKPOYLLENLPLSGVPFNPPTSPTNTTLLK 490

Db 653 PEAVDPLMRAAKTV-----NFGVLYGMSAHLRSQEL--AIPVEEA----- 691

QY 491 IKVMTTLGWDKAFSKRHFDFL 511

Db 692 -----VAFIERVQSF 702

RESULT 15

US-08-384-490-31

; Sequence 31, Application US/08384490

; Patent No. 5618711

; GENERAL INFORMATION:

; APPLICANT: Gelfand, David H.

; APPLICANT: Lawler, Susanne

; TITLE OF INVENTION: Recombinant Expression Vectors and

; TITLE OF INVENTION: Purification Methods for Thermus Thermophilus DNA

; TITLE OF INVENTION: Polymerase

; NUMBER OF SEQUENCES: 31

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Hoffmann-La Roche Inc.

; STREET: 340 Kingsland Street

; CITY: Nutley

; STATE: New Jersey

; COUNTRY: U.S.A.

; ZIP: 07110

; COMPUTER READABLE FORM: disk

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/384,490

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/148,133

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Sias, Stacey R.

; REGISTRATION NUMBER: 32,630

; REFERENCE/DOCKET NUMBER: 8867

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (510) 814-2863

; TELEFAX: (510) 814-2977

; INFORMATION FOR SEQ ID NO: 31:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 834 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; US-08-384-490-31

Query Match 3.1%; Score 104.5; DB 1; Length 834;

Best Local Similarity 18.5%; Pred. No. 1.9;
Matches 115; Conservative 86; Mismatches 191; Indels 229; Gaps 30;

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QY 14 GDPEQDL-----VGEVFTIYSENERMSAEGLLKFLHTEQGDVDFTLDDAK--QIMERIR- 65
Db 188 GDFSDNLPGVKIGKGTALKLLKEMGSLENLLK-----NLDVRKPNVREKIK 236
QY 66 --KDWKKSFGLASINSDL-----SKEAFKYLMPDLNGVLHNVVHODMTQPM 111
Db 237 HLEDRLSLELSRVITDLPLEVDLAOGREPDREGLRAFLERLEFGSLLHEFGLEAPL 296
QY 112 SHYFTGHSYLTGNSLSSDSDPTAAALRGVGVVVDLWDDKGGKMKVTHGNTITN 171
Db 297 -----EAP-----WPPPEGAFV---GFVLSR 315
QY 172 PVSF---OKCVTAKNNAFTSEYPCVVTIEDHLTSELOHAA-----EILEQILG 219
Db 316 PEPWAELKALACRGRVHRAADPL-AGLKD--LKEVGGLLAKDLAVLASREGLDLVP 372
QY 220 DALYPPPTDALVEFPPS---PESLKRKIIISTKPKKEYLEACSTQKLAEE--NRNLVEEL 274
Db 373 D-----DPMILAVLLDPSNTTPEGVARRY-----GGWETEDAAHRAALLSERLHRLKRL 422
QY 275 EKEDKL-----EOTTAPLEENHI-----LGENTPSIRKEVEVLSOK 311
Db 423 EGEEKLLWLYHVEKPLSRVLAHMEATGVRLDVAYLQALSLELAEEIRLEEEVEFLA-- 480
QY 312 EMSTPAELNSRSPSD-----LGEATSTRYSKSDGNDNDNPKHFKYARLITIRAK 360
Db 481 --GHPFNLSRDQLERVLFDLRLPALGKTQKT--GKRSTSAVLEALREAHPIVEKILQ 536
QY 361 HAKGTSMEH-----RL-----QVDESVKRISLSSEKLEKVEK----- 393
Db 537 HRELTCLKNTVVDPLPSLVHPRTGRLHTRFNQTATATGRLSDDPNLQNPVTPPLGQRI 596
QY 394 -----WPEALVFTQ-----KNILRVYPAANRVNNSNFCPTLAWNYGA- 431
Db 597 RRAFAAGWALVALDYISOELRVLAHLSGDENLIRVFOEGKDIHTQ-----TASWMEGVP 652
QY 432 -QWVAQNMOGYGKELWQAFGKFGKGGCGYVLKPOYLLLENLPSGVFPNPTSPRNTTILK 490
Db 653 PEAVDPLMRRAAKTV-----NFGVLYGMSAHLRSOEL--AIPYEA----- 691
QY 491 IKVMTTLGWDKAFSRHFDLF 511
Db 692 -----VAFIERVQSF 702
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Search completed: July 26, 2002, 17:22:14
Job time: 4897 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 26, 2002, 15:57:57 ; Search time 37.97 seconds
(without alignments)
1589.257 Million cell updates/sec

Title: US-09-828-447-12
Perfect score: 3228
Sequence: 1 MCSACRSGTPKGDPEQDL.....MLPHFOCKCTFQDTAPISS 628

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1338	40.2	553	T06771	phosphoinositide-s
2	1293	38.9	549	T11688	phosphoinositide-s
3	1251.5	37.6	600	T06775	phosphoinositide-s
4	1241.5	37.3	600	T06420	phosphoinositide-s
5	1234	37.1	551	T06777	phosphoinositide-s
6	1225.5	36.8	585	T07425	phosphoinositide-s
7	1219.5	36.6	594	T06467	phosphoinositide-s
8	1202.5	36.1	581	T50841	phosphoinositide-s
9	1194	35.9	605	T50842	phospholipase C2 l
10	1192.5	35.8	565	T07424	phosphoinositide-s
11	1175	35.3	596	T07421	phosphoinositide-s
12	1171.5	35.2	581	S71170	phosphoinositide-s
13	1165	35.0	586	T50843	phospholipase C1 l
14	1155	34.7	584	T49206	phosphoinositide-s
15	1030.5	31.0	526	T05681	phosphoinositide-s
16	748	22.5	531	S54098	1-phosphatidylinos
17	692	20.8	764	S14113	1-phosphatidylinos
18	680.5	20.4	513	T45658	1-phosphatidylinos
19	623.5	18.7	751	T29357	1-phosphatidylinos
20	603.5	18.1	745	PC4183	1-phosphatidylinos
21	600	18.0	801	A44165	1-phosphatidylinos
22	594.5	17.9	709	C28821	1-phosphatidylinos
23	594.5	17.9	756	B28821	1-phosphatidylinos
24	577.5	17.4	756	A55943	1-phosphatidylinos
25	566.5	17.0	895	T32374	hypothetical prote
26	561	16.9	997	T54390	phosphoinositide-s
27	559	16.8	1096	I562358	inositol 1,4,5-tri
28	549.5	16.5	1023	B38932	phospholipase C (E
29	541.5	16.3	1211	S68251	phospholipase C, l

30	535	16.1	1181	2	A43346	1-phosphatidylinos
31	520.5	15.6	1095	1	A31225	phospholipase C (E
32	520	15.6	1176	1	A48047	phospholipase C (E
33	519.5	15.6	1898	2	T42440	phospholipase C ho
34	517	15.5	1210	2	A48001	phospholipase C (E
35	512	15.4	1922	2	T21581	hypothetical prote
36	504.5	15.2	1216	2	A28822	1-phosphatidylinos
37	499.5	15.0	1217	2	A45493	phospholipase C-be
38	499	15.0	1216	2	A28821	1-phosphatidylinos
39	498	15.0	1299	2	T24239	hypothetical prote
40	495	14.9	1051	2	S27002	phospholipase C (E
41	495	14.9	1234	2	S52099	phospholipase C-be
42	495	14.9	1234	2	I38994	phospholipase C-be
43	492	14.8	1418	2	T37264	phospholipase C (E
44	490	14.7	875	1	S66672	phosphatidylinosit
45	482	14.5	1173	1	A53430	1-phosphatidylinos

ALIGNMENTS

RESULT 1

T06771

phosphoinositide-specific phospholipase C (EC 3.1.4.-) P12 - soybean
C:Species: Glycine max (soybean)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999

C:Accession: T06771

R:Shi, J.; Gonzales, R.A.; Bhattacharyya, M.K.

submitted to the EMBL Data Library, November 1995

A:Description: Phosphoinositide-specific phospholipase Cs contain a C-terminal domain

A:Reference number: Z15800

A:Accession: T06771

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-553 <SHI>

A:Cross-references: EMBL:U41473; NID:g1399302; PIDN:AB03257.1; PID:g1399303
A:Experimental source: cultivar Williams 82; etiolated hypocotyls

A:Superfamily: Arabidopsis thaliana 1-phosphatidylinositol-4,5-bisphosphate phosphodi

phosphatase phosphodiesterase domain Y homology

C:Keywords: phosphoric diester hydrolase

F:81-223/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain x h

Query Match 40.2%; Score 1338; DB 2; Length 553;

Best Local Similarity 47.9%; Pred. No. 1.5e-77;

Matches 282; Conservative 85; Mismatches 176; Indels 46; Gaps 11;

QY 34 MSAGLLKFLHTEQGDVDTLDDAKQIMERIRKDKKKSFGGLASI-----NSDLSKEAF 86

DB 1 MSADQLRLFLHDHORETDCSAEDSNRILDSIIQSRKQNDTNAECDHHTDNNNGLSLDEF 60

QY 87 RYLMNPDLNGVLHNVVHODMTQPMSHVFIFTGHSYLTGNOLSSDSDPTIAAALRGV 146

DB 61 FRFLVLDVNDPLKQSVHDDMAPLSHFYIYGHNSYLTGNOLSSDSDVPIIKALQGV 120

QY 147 RVVELDLWDD-KGGMKVTHGNTLNPVSFQKCVTAIKNNAFFTSEYPCVVTIEDHLTSE 205

DB 121 RVIELDLPNSTKDDIDVVHGRTLTAPVSLIQLSKSIKSEYAFVKSVDYPIITLEDHLTPF 180

QY 206 LQGHAAIEQLGALYPPPTDALVEPPSPESLKRKIIISTKPKVEYLEACSTQKLM 265

DB 181 LQAKVAEMTAQVFGMDLXF-POADSLTEPTTPELTKGRILLISTKPKVEYLE- 231

QY 266 ENRNLEVELEKEDKLEQTTFAPLEENHILGENTPSLREVEVLSQKEMSTPAELNSRPS 325

DB 232 -----KQFKDSEREST-----EE-----GSLSPCPIPELEAVDEK-----LANG---S 267

QY 326 DLGEATSTRYSKNDGNDNPKHKFKYARLITIRLAKHAKTSMEHRLQVDESVKRLSLSES 385

DB 268 DLDEGLNARDKKSQDSAP---EYKRLTIIHAGK-PKG-HVKHLNNVGGVKRLSLSEQ 322

QY 386 KLEKVVKEPEALVKFTQKNILRVYPAANRVNSSFNCFPTLAWNYGAQVVAQNMQGYKREL 445

Db 323 ELEKASATYGSIDIVRFTQKNLIIRVYPKGRVTSNYPHIGMYGAOMVAFNMOGHSKSL 382
QY 446 WQAFKFKGNGGGYVVKLPYLLNLELSPGVFPNPTSPRNTTLILKIKVMTTLGWDKAFSK 505
Db 383 WYMQGFRANGGGYVVKKPAFLIEKPHNEVDFPKRALPKYKTLKVKYMGNGWSSDFS 442
QY 506 RHFDLSPDFRTRVIVGVPADEAKWKTSVVNSWAPHNEDEHFAKCPALALLRIEV 565
Db 443 THDFSFPDFYTKVCIIVGVPADEAKWKTIVQDNWFPVWDEFEFPLTVPALALLRIEV 502
QY 566 RDHDDSKDEFEGOTCLPIHEVRDGYRCMOMYDKGNVKGVLMLPHEQ 614
Db 503 REYDKHEKDDFGGOTCLPISELRSKGFRAVFLDQKGBQLKSVKLLMRQ 551
RESULT 2
T06775
phosphoinositide-specific phospholipase C (EC 3.1.4.-) - cowpea
C:Species: Vigna unguiculata (cowpea)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jan-2000
C:Accession: T11688
R:Pham Thi, A.T.; El Maarouf, H.; Gareil, M.; d'Arcy-Lameta, A.; Zuily-Fodil, Y.
submitted to the EMBL Data Library, January 1997
A:Description: Molecular cloning and expression of a phosphoinositide-specific phospholipase C from cowpea
A:Reference number: Z17316
A:Accession: T11688
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-549 <PHA>
A:Cross-references: EMBL:U85250; NID:g1786114; PID:g1786115
A:Experimental source: cultivar EPAGE-1; leaves; clone C7b
C:Genetics:
A:Gene: PLC1
C:Superfamily: Arabidopsis thaliana 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain
C:Keywords: phosphodiesterase domain Y homology
F:106-248/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain x hom

Query Match 38.9%; Score 1293; DB 2; Length 549;
Best Local Similarity 44.9%; Pred. No. 1.1e-74;
Matches 272; Conservative 85; Mismatches 167; Indels 82; Gaps 10;
QY 12 PKGDPQDLVGEVFTIYSEN-ERMSAGLLKFLHTEQGVDFTLDDAKQIMERIRK-DWK 69
Db 21 PKPPDP---VQKAFSEFSGCASSMSAEHLRLFLAEHQGEVDCVTSDSEQLQQRKEDGE 77
QY 70 KSPGLASINSLSKAEAFKRYLMPDLNGVLHNVVHODMTQPMHSYFTFGHNSYLTGNOL 129
Db 78 TGFDL-----HDFHFLQENDLNVLPKSOVHHDMNAPLSHYFTYGHNSYLTGNOL 128
QY 130 SSDSDTPIAALRRGVVVELDLMPD-DKGMKVTHTGNTLNPVSKCVTAIKNNAPF 188
Db 129 SSDSDAPIIKALQGVVRIELDLWPNKNDIDVVHGRTLTPVSLRLCLASIKREYAFV 188
QY 189 TSEYPCVTVIEDHLSLSELOCHAEILQILGDALYPTPTDALVEFPSPESLKRKIIST 248
Db 189 KSOYPLVITLEDHLTPDLQAKVATQVGFELLY-PQDLSLTFEFPSPESLKGRIIST 247
QY 249 KPPKEYLEACSTQKLA MENRLVEELEKEDKLEQTTFAPLEENHILGENTPSPSRKEVEVL 308
Db 248 KPPKEFLES----- 256
QY 309 SOKEMSTPAELNSRSPDLGEATSTRYSKSDNGDNPKHFKYARLITIRLAKHAKGTSM 368
Db 257 SEKESAE-----EVSLSRENADERTONKRAPEYKRLITTHAGK-PKG-BIQ 301
QY 369 HRLQVDESVKRISLSSEKLEKVVKEKPEALVKFTOKNIRLVYPAANRVNSNFCPTLAWN 428
Db 302 DELKAAGNVRRLSLSEQALEKASESYGADVRFTHNNILRVYPKCTRLNNSNYKPHICWT 361
QY 429 YGAQVVAONMOCYKELWQAFKFKGNGGGYVVKLPYLLNLELSPGVFPNPTSPRNTTLI 488

Db 362 YGAQVVAONMOCYKELWQAFKFKGNGGGYVVKLPYLLNLELSPGVFPNPTSPRNTTLI 421
QY 489 LKIKVMTTLGWDKAFSKRHFDFLSPDFRTRVIVGVPADEAKWKTSVVNSWAPHNEDE 548
Db 422 LKVKYVILGKWSLDESPDFSYSPDFYVVCIVGVPADEIKKKTSTVISNWFVWNEE 481
QY 549 HEFALKCPALALLRIEVDRHDDSKDEFEGOTCLPIHEVRDGYRCMOMYDKGNVKGVL 608
Db 482 DFPLTVPALALLRIEVDRHDDSKDEFEGOTCLPISELRSKGFRAVFLDQKGBQLKSVK 541
QY 609 MLFHFQ 614
Db 542 LLMRFQ 547
RESULT 3
T06775
phosphoinositide-specific phospholipase C (EC 3.1.4.-) P13 (clone SPM537) - soybean
C:Species: Glycine max (soybean)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999
C:Accession: T06775
R:Shi, J.; Gonzales, R.A.; Bhattacharyya, M.K.
submitted to the EMBL Data Library, November 1995
A:Description: Phosphoinositide-specific phospholipase Cs contain a C-terminal domain
A:Reference number: Z15800
A:Accession: T06775
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-600 <SHI>
A:Cross-references: EMBL:U41474; NID:g1399304; PID:AA03258.1; PID:g1399305
A:Experimental source: cultivar Williams 82; etiolated hypocotyls
C:Superfamily: Arabidopsis thaliana 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain Y homology
C:Keywords: phosphodiesterase domain Y homology
F:108-250/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain x hom

Query Match 37.6%; Score 1251.5; DB 2; Length 600;
Best Local Similarity 45.8%; Pred. No. 5.5e-72;
Matches 272; Conservative 89; Mismatches 202; Indels 31; Gaps 12;
QY 24 VFTIYSENERMSAGLLKFLHTEQGVDFTLDDAKQIMERIRKDWKKSFGLASINSLSK 83
Db 31 LFNEYSENELMTPSHLKRFLVDVQKAEEDAQAALIDSFRHFRHRRGAG-----LNL 83
QY 84 EAFKRYLMPDLNGVL-HNVVHODMTQPMHSYFTFGHNSYLTGNOLSSSDTPIAAL 142
Db 84 ETPFKYLSDDNPPLPSHGVDHMTPLSHYFTYGHNSYLTGNOLSSDCSDVPIINAL 143
QY 143 RGVVVELDLMPD-DKGMKVTHTGNTLNPVSKCVTAIKNNAPFTSEYPCVTVIEDH 201
Db 144 KGVVRIELDLWPNASKDSIDLHGRTLTPVLEIRCLRSIKDHAFVASEYPPVITLEDH 203
QY 202 LTSELOCHAEILQILGDALYPTPTDALVEFPSPESLKRKIISTKPKPEYLEACSTQ 261
Db 204 LTPDLQAKVATQVGFELLY-FTPNSESVKPEFPSPESLKRKIISTKPKPEYLEAKE 262
QY 262 KLA MENRLVEELEKEDKLEQTTFAPLEENHILGENTPSPSRKEVEVLSQEMSTPAELNS 321
Db 263 K-----GDSQHEKEKGGDSEHGKAS--GEDEAMGKEVPSL-KGGTIDYKDNVDEDLND 315
QY 322 RSPDLSGEATSTRYSKSDNGDNPKHFKYARLITIRLAKHAKGTSMHRLQVD-ESVKRI 380
Db 316 EEEFD-----ESDKSHHNEAP---EYRHLTAIHAGK-PKGLVE-CLKVDPEKVRRL 362
QY 381 SLSEKLEKVVKEKPEALVKFTOKNIRLVYPAANRVNSNFCPTLAWNQAQVVAONMOC 440
Db 363 SLSEQLEKAAINYGQIVRFTORNIILRVYPKCTRLNNSNYKPHICWT 422
QY 441 YGELWQAFKFKGNGGGYVVKLPYLLNLELSPGVFPNPTSPRNTTLILKIKVMTTLGWD 500
Db 423 YGRLWLHMHGFRANGCGGYVVKLPYLLNLELSPGVFPNPTSPRNTTLILKIKVMTTLGWD 482

QY 501 KAFSRHFDLSPDPDFTRVIVGVPADEAKKTSVNDNSWAPHWNEDHEFALKCPAL 560
 Db 483 YDEKHTHFDQYSPDFTYTRVGTAGVNDTMRKTRKAIEDNWLPTWNEAFEPPLTPAL 542
 QY 561 LRLEVHDDHDSKDEFGTCLPIHEVRDGRYRCMOMYDKGNVLKGNVLMFLHFQ 614
 Db 543 LRLEVHDDHDSKDEFGTCLPIHEVRDGRYRCMOMYDKGNVLKGNVLMFLHFQ 596

RESULT 4

T06420
 phosphoinositide-specific phospholipase C (EC 3.1.4.-), plasma membrane-associated - soybean
 N:Alternate names: phosphatidylinositol-specific phospholipase C
 C:Species: Glycine max (soybean)
 C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999

C:Accession: T06420
 R:Shi, J.; Gonzales, R.A.; Bhattacharyya, M.K.
 submitted to the EMBL Data Library, April 1995

A:Description: Characterization of a soybean cDNA that encodes a novel plasma membrane
 A:Reference number: Z15665
 A:Accession: T06420
 A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA
 A:Residues: 1-600 <SHI>
 A:Cross-references: EMBL:U25027; NID:G945038; PIDN:AAA74441.1; PID:G945039

A:Experimental source: cv. Williams 82; etiolated hypocotyls
 C:Superfamily: Arabidopsis thaliana 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain Y homolog
 C:Keywords: phosphoric diester hydrolase

F:108-250/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X hom

Query Match 37.3%; Score 1241.5; DB 2; Length 600;
 Best Local Similarity 45.3%; Pred. No. 2.4e-71;
 Matches 269; Conservative 89; Mismatches 205; Indels 31; Gaps 11;

QY 24 VFTIYSENERMSAEGLLFLTEQGVDFTLDDAKQIMERIRKDKKSGFLASINDLSK 83
 Db 31 LFEETSENEFWTPSHLKLFLVEVQEKATEDEAQAIDSFHFRGAG-----LNL 83

QY 84 EAFRYLMNPDLNGYL-HNHYVDQMTQPMGSHYFTFTGHSNYLTGNQSDSDSTPIAAL 142
 Db 84 EFTFYKFLSDNPPLPSGHVHDMTLP SHYFTFTGHSNYLTGNQSDSDSTPIAAL 143

QY 143 RGVVVELDLPD-DKGGKVTGNTLTPVSKFCVTAIKNNAFTSEYPCVVTIEDH 201
 Db 144 KRGVRVIELDLPNASNDNDVLRGTLTPVELIRCLRSIKDHAFVASEYPVVITLEDH 203

QY 202 LTSELOGHAAIBLQILGALYPTTDALVFPSPESLKKIITSTPKPEYLEACSTQ 261
 Db 204 LTPOLQAKVAMVTETFGD-LLETPNSVSKFEPSPESLKKIITSTPKPEYLEAKE 262

QY 262 KAMENNLVVEELEKEDKLEQTFAPLENHILGENTPSPSRKEVEVLQKEMSTPAELNS 321
 Db 263 K-----GDSQHEKEGDDSOHG--KALGDEAWGKEVPSL-KGGTIEDYKDYNDVDLND 315

QY 322 RSPSDLGATSTRYSKSDNDGNPNKHFYARLITIRLAKHAKGTSMEHRLQVD-ESVKRI 380
 Db 316 EEFDF-----ESDKSHNEAP---EYRLIAHAGKPKGG--LAECCLKVDPKVRRL 362

QY 381 SLSESLEKLVKVEKPEALVFTQKILRYVYPANRVNSNFCPTLANNYGAQVAMNMQG 440
 Db 363 SLSEQLKEAANHQGQIVRTFORNLRYPKGRTRIDSSNYPNLIQWGHGAQVAFNMQG 422

QY 441 YGKELWQAFKFGKNGCGGYLVKFOYLLLENLPSCVPPNPTSPRNTTLILKIKVITLGD 500
 Db 423 YGRSLWLMHGMFRANGCGGYVKKPNFLETCGPDDEVENPKAKLPVKTTLKVITYMGEWY 482

QY 501 KAFSRHFDLSPDPDFTRVIVGVPADEAKKTSVNDNSWAPHWNEDHEFALKCPAL 560
 Db 483 YDEKHTHFDQYSPDFTYTRVGTAGVNDTMRKTRKAIEDNWLPTWNEAFEPPLTPAL 542

QY 561 LRLEVHDDHDSKDEFGTCLPIHEVRDGRYRCMOMYDKGNVLKGNVLMFLHFQ 614

Db 543 LRLEVHDDHDSKDEFGTCLPIHEVRDGRYRCMOMYDKGNVLKGNVLMFLHFQ 596

RESULT 5

T06777

phosphoinositide-specific phospholipase C (EC 3.1.4.-) P25 (clone SPM537) - soybean
 C:Species: Glycine max (soybean)
 C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999

C:Accession: T06777
 R:Shi, J.; Gonzales, R.A.; Bhattacharyya, M.K.
 submitted to the EMBL Data Library, November 1995

A:Description: Phosphoinositide-specific phospholipase Cs contain a C-terminal domain
 A:Reference number: Z15800
 A:Accession: T06777
 A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA
 A:Residues: 1-551 <SHI>
 A:Cross-references: EMBL:U41475; NID:G1399306; PIDN:AAB03259.1; PID:G1399307

A:Experimental source: cultivar Williams 82; etiolated hypocotyls
 C:Superfamily: Arabidopsis thaliana 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain Y homolog
 C:Keywords: phosphoric diester hydrolase

F:70-212/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X h

Query Match 37.1%; Score 1234; DB 2; Length 551;
 Best Local Similarity 45.4%; Pred. No. 6.3e-71;
 Matches 272; Conservative 88; Mismatches 171; Indels 68; Gaps 16;

QY 34 MSAGLLKFLHTEQGVDFTLDDAKQIMERIRKDKKSGFLASINDLSKFAFRKYL-- 91
 Db 1 MTATPLRSFLAEVQREDNATEEAQALI-----DGHKHLSTFH-RSGUNLESFTNYLF 54

QY 92 --NPDNLGVHNVVDQMTQPMGSHYFTFTGHSNYLTGNQSDSDSTPIAALRGVRV 149
 Db 55 HNNPPLPSLG--VHDMSPSLSHYFTFTGHSNYLTGNQSDSDSTPIAALRGVRV 112

QY 150 ELDLWDD-DKGGKVTGNTLTPVSKFCVTAIKNNAFTSEYPCVVTIEDHLSLQ 208
 Db 113 ELDIWPNESKNDVNLHGRTLTPVELIRCLRSIKDHAFVASEYPVVITLEDHLDLQ 172

QY 209 HAAEILEQILGALYPTTDALVFPSPESLKKIITSTPKPEYLEACSTOKLAME 268
 Db 173 KVAEMITQTFGDL-FAPTSLSLKEFPSPESLKKIITSTPKPEYLEAKEVQ----- 224

QY 269 NLVEELEKEDKLEQTFAPLENHILGENTPSPSRKEVEVLQKEMSTPAE 318
 Db 225 -----EKEEESQOB--KPADDEAWGKEVPSLRGGTISDYKNIEDDVLDDDE----- 270

QY 319 LNSRSPDLGATSTRYSKSDNDGNPNKHFYARLITIRLAKHAKGTSMEHRLQVD-BSV 377
 Db 271 -----DIDEAKSRQDADE-----YRLIAHAGKPKGG--LTECLKVDPK 312

QY 378 KRISLESLEKLVKVEKPEALVFTQKILRYVYPANRVNSNFCPTLANNYGAQVAM 437
 Db 313 RLSELSLEKLEKAAETGKBEIVRTFORNLRYPKGRTRITSTNYNPLIGWGHGAQVAFN 372

QY 438 MQGYGKELWQAFKFGKNGCGGYLVKFOYLLLENLPSCVPPNPTSPRNTTLILKIKV 495
 Db 373 MQGYGRSLWLMHGMFRANGCGGYVKKPNFLETCGPDDEVENPKAKLPVKTT--LKVTI 430

QY 496 TLGWDAKAFSRHFDLSPDPDFTRVIVGVPADEAKKTSVNDNSWAPHWNEDHEFALK 555
 Db 431 GEGWFLDFKHTHFDQYSPDFTYTRVGTAGVNDTMRKTRKAIEDNWLPTWNEAFEP 490

QY 556 PELALLRIEVRDHDHDSKDEFGTCLPIHEVRDGRYRCMOMYDKGNVLKGNVLMFLHFQ 614
 Db 491 PELALLRIEVRDHDHDSKDEFGTCLPIHEVRDGRYRCMOMYDKGNVLKGNVLMFLHFQ 549

RESULT 6
 T07425

us-09-828-447-12.rpr

Sun Jul 28 10:34:36 2002

phosphoinositide-specific phospholipase C (EC 3.1.4.-) - garden pea

N: Alternate names: phospholipase C
 C: Species: Pisum sativum (garden pea)
 C: Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 20-Jun-2000
 C: Accession: T06467

R: Reddy, M.K. submitted to the EMBL Data Library, October 1997

A: Gene: plc3

A: Reference number: Z15699

A: Accession: T06467

A: Status: translated from GB/EMBL/DBJ

A: Molecule type: mRNA

A: Residues: 1-594 <RED>

A: Cross-references: EMBL:Y15253; PIDN:CAA75546.1

A: Note: plc

C: Genes: plc

C: Superfamily: Arabidopsis thaliana 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain Y homolog

C: Superfamily: phosphodiesterase domain Y homolog

C: Keywords: phosphoric diester hydrolase

C: Keywords: phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X

F: 112-254/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X homolog

Query Match 36.6%; Score 1219.5; DB 2; Length 594;

Best Local Similarity 44.9%; Pred. No. 5.9e-70;

Matches 272; Conservative 100; Mismatches 187; Indels 47; Gaps 17;

Query Match 36.6%; Score 1219.5; DB 2; Length 594;

Best Local Similarity 44.9%; Pred. No. 5.9e-70;

Matches 272; Conservative 100; Mismatches 187; Indels 47; Gaps 17;

Query Match 36.6%; Score 1219.5; DB 2; Length 594;

Best Local Similarity 44.9%; Pred. No. 5.9e-70;

Matches 272; Conservative 100; Mismatches 187; Indels 47; Gaps 17;

Query Match 36.6%; Score 1219.5; DB 2; Length 594;

Best Local Similarity 44.9%; Pred. No. 5.9e-70;

Matches 272; Conservative 100; Mismatches 187; Indels 47; Gaps 17;

Query Match 36.6%; Score 1219.5; DB 2; Length 594;

Best Local Similarity 44.9%; Pred. No. 5.9e-70;

Matches 272; Conservative 100; Mismatches 187; Indels 47; Gaps 17;

Query Match 36.6%; Score 1219.5; DB 2; Length 594;

Best Local Similarity 44.9%; Pred. No. 5.9e-70;

Matches 272; Conservative 100; Mismatches 187; Indels 47; Gaps 17;

Query Match 36.6%; Score 1219.5; DB 2; Length 594;

Best Local Similarity 44.9%; Pred. No. 5.9e-70;

Matches 272; Conservative 100; Mismatches 187; Indels 47; Gaps 17;

Query Match 36.6%; Score 1219.5; DB 2; Length 594;

Best Local Similarity 44.9%; Pred. No. 5.9e-70;

Matches 272; Conservative 100; Mismatches 187; Indels 47; Gaps 17;

Query Match 36.6%; Score 1219.5; DB 2; Length 594;

Best Local Similarity 44.9%; Pred. No. 5.9e-70;

Matches 272; Conservative 100; Mismatches 187; Indels 47; Gaps 17;

Query Match 36.6%; Score 1219.5; DB 2; Length 594;

Best Local Similarity 44.9%; Pred. No. 5.9e-70;

Matches 272; Conservative 100; Mismatches 187; Indels 47; Gaps 17;

Query Match 36.6%; Score 1219.5; DB 2; Length 594;

Best Local Similarity 44.9%; Pred. No. 5.9e-70;

Matches 272; Conservative 100; Mismatches 187; Indels 47; Gaps 17;

Query Match 36.6%; Score 1219.5; DB 2; Length 594;

Best Local Similarity 44.9%; Pred. No. 5.9e-70;

Matches 272; Conservative 100; Mismatches 187; Indels 47; Gaps 17;

Query Match 36.6%; Score 1219.5; DB 2; Length 594;

Best Local Similarity 44.9%; Pred. No. 5.9e-70;

Matches 272; Conservative 100; Mismatches 187; Indels 47; Gaps 17;

Query Match 36.6%; Score 1219.5; DB 2; Length 594;

Best Local Similarity 44.9%; Pred. No. 5.9e-70;

Matches 272; Conservative 100; Mismatches 187; Indels 47; Gaps 17;

Query Match 36.6%; Score 1219.5; DB 2; Length 594;

Best Local Similarity 44.9%; Pred. No. 5.9e-70;

Matches 272; Conservative 100; Mismatches 187; Indels 47; Gaps 17;

Query Match 36.6%; Score 1219.5; DB 2; Length 594;

Best Local Similarity 44.9%; Pred. No. 5.9e-70;

Matches 272; Conservative 100; Mismatches 187; Indels 47; Gaps 17;

Query Match 36.6%; Score 1219.5; DB 2; Length 594;

Best Local Similarity 44.9%; Pred. No. 5.9e-70;

Matches 272; Conservative 100; Mismatches 187; Indels 47; Gaps 17;

Query Match 36.6%; Score 1219.5; DB 2; Length 594;

Best Local Similarity 44.9%; Pred. No. 5.9e-70;

Matches 272; Conservative 100; Mismatches 187; Indels 47; Gaps 17;

phosphoinositide-specific phospholipase C (EC 3.1.4.-) plc3 - potato

C: Species: Solanum tuberosum (potato)
 C: Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
 C: Accession: T07425

R: Kopka, J.; Pical, C.; Gray, J.E.; Mueller-Roeber, B.

A: Gene: plc3

A: Reference number: Z16026; MUID: 98111496

A: Accession: T07425

A: Status: translated from GB/EMBL/DBJ

A: Molecule type: mRNA

A: Residues: 1-585 <KOP>

A: Cross-references: EMBL:X94289; NID:g2853038; PIDN:CAA63954.1; PID:g2853039

A: Note: plc3

C: Genes: plc3

C: Superfamily: Arabidopsis thaliana 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain Y homolog

C: Superfamily: phosphodiesterase domain Y homolog

C: Keywords: phosphoric diester hydrolase

C: Keywords: phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X homolog

F: 111-252/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X homolog

Query Match 36.8%; Score 1225.5; DB 2; Length 585;

Best Local Similarity 44.2%; Pred. No. 2.4e-70;

Matches 268; Conservative 90; Mismatches 187; Indels 61; Gaps 14;

Query Match 36.8%; Score 1225.5; DB 2; Length 585;

Best Local Similarity 44.2%; Pred. No. 2.4e-70;

Matches 268; Conservative 90; Mismatches 187; Indels 61; Gaps 14;

Query Match 36.8%; Score 1225.5; DB 2; Length 585;

Best Local Similarity 44.2%; Pred. No. 2.4e-70;

Matches 268; Conservative 90; Mismatches 187; Indels 61; Gaps 14;

Query Match 36.8%; Score 1225.5; DB 2; Length 585;

Best Local Similarity 44.2%; Pred. No. 2.4e-70;

Matches 268; Conservative 90; Mismatches 187; Indels 61; Gaps 14;

Query Match 36.8%; Score 1225.5; DB 2; Length 585;

Best Local Similarity 44.2%; Pred. No. 2.4e-70;

Matches 268; Conservative 90; Mismatches 187; Indels 61; Gaps 14;

Query Match 36.8%; Score 1225.5; DB 2; Length 585;

Best Local Similarity 44.2%; Pred. No. 2.4e-70;

Matches 268; Conservative 90; Mismatches 187; Indels 61; Gaps 14;

Query Match 36.8%; Score 1225.5; DB 2; Length 585;

Best Local Similarity 44.2%; Pred. No. 2.4e-70;

Matches 268; Conservative 90; Mismatches 187; Indels 61; Gaps 14;

Query Match 36.8%; Score 1225.5; DB 2; Length 585;

Best Local Similarity 44.2%; Pred. No. 2.4e-70;

Matches 268; Conservative 90; Mismatches 187; Indels 61; Gaps 14;

Query Match 36.8%; Score 1225.5; DB 2; Length 585;

Best Local Similarity 44.2%; Pred. No. 2.4e-70;

Matches 268; Conservative 90; Mismatches 187; Indels 61; Gaps 14;

Query Match 36.8%; Score 1225.5; DB 2; Length 585;

Best Local Similarity 44.2%; Pred. No. 2.4e-70;

Matches 268; Conservative 90; Mismatches 187; Indels 61; Gaps 14;

Query Match 36.8%; Score 1225.5; DB 2; Length 585;

Best Local Similarity 44.2%; Pred. No. 2.4e-70;

Matches 268; Conservative 90; Mismatches 187; Indels 61; Gaps 14;

Query Match 36.8%; Score 1225.5; DB 2; Length 585;

Best Local Similarity 44.2%; Pred. No. 2.4e-70;

Matches 268; Conservative 90; Mismatches 187; Indels 61; Gaps 14;

Query Match 36.8%; Score 1225.5; DB 2; Length 585;

Best Local Similarity 44.2%; Pred. No. 2.4e-70;

Matches 268; Conservative 90; Mismatches 187; Indels 61; Gaps 14;

Query Match 36.8%; Score 1225.5; DB 2; Length 585;

Best Local Similarity 44.2%; Pred. No. 2.4e-70;

Matches 268; Conservative 90; Mismatches 187; Indels 61; Gaps 14;

Query Match 36.8%; Score 1225.5; DB 2; Length 585;

Best Local Similarity 44.2%; Pred. No. 2.4e-70;

Matches 268; Conservative 90; Mismatches 187; Indels 61; Gaps 14;

Query Match 36.8%; Score 1225.5; DB 2; Length 585;

Best Local Similarity 44.2%; Pred. No. 2.4e-70;

Matches 268; Conservative 90; Mismatches 187; Indels 61; Gaps 14;

Query Match 36.8%; Score 1225.5; DB 2; Length 585;

Best Local Similarity 44.2%; Pred. No. 2.4e-70;

Matches 268; Conservative 90; Mismatches 187; Indels 61; Gaps 14;

Query Match 36.8%; Score 1225.5; DB 2; Length 585;

Best Local Similarity 44.2%; Pred. No. 2.4e-70;

Matches 268; Conservative 90; Mismatches 187; Indels 61; Gaps 14;

Query Match 36.8%; Score 1225.5; DB 2; Length 585;

Best Local Similarity 44.2%; Pred. No. 2.4e-70;

Matches 268; Conservative 90; Mismatches 187; Indels 61; Gaps 14;

RESULT 8

T50841

phosphoinositide-specific phospholipase C (EC 3.1.4.-) [imported] - rape

RESULT 7

T06467

RESULT 9
T50842
phospholipase C2 [imported] - common tobacco
C; Species: Nicotiana tabacum (common tobacco)

RESULT 10
T07424
phosphatidylcholine-specific phospholipase C (EC 3.1.4.-) plc2 - potato
C.Species: Solanum tuberosum (potato)
C.Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
C.Accession: T07424
R.Kopka, J.; Pical, C.; Gray, J.E.; Mueller-Roeber, B.

R:Kopka, J.; Pical, C.; Gray, J.E.; Mueller-Roeber, B.
Plant Physiol. 116, 239-250, 1998
A:Title: Molecular and enzymatic characterization of three phosphoinositide-specific
A:Reference number: Z16026; MUID:98111496
A:Accession: T07421
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-596 <KOP>
A:Cross-references: EMBL:X93564; NID:g2853040; PIDN:CAA63777.1; PID:g2853041
A:Experimental source: cv. Desiree
C:Genetics:
A:Gene: PLC1
C:Superfamily: Arabidopsis thaliana 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain Y homology
A:Keywords: phosphoric diester hydrolase
F:113-253/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X homology

Query Match 35.3%; Score 1175; DB 2; Length 596;
Best Local Similarity 42.2%; Pred. No. 4.1e-67;
Matches 261; Conservative 100; Mismatches 221; Indels 36; Gaps 12;
QY 6 CC--RSSTPKGPEODLVCEVFTIYSENERMSAEGLLKFLHTEQGDVDFTLDDAKQIMER 63
DB 9 CCFORFKLKEAEPDEIKDLFERSENGIMTAHEHLCKFLKDVQGEENVTKKEAEYTES 68
QY 64 IRDKMKKSGFLASINSDLSKEAFKRYLMNPDNLGV--HNVVHODMTOPMSHYFTIGHN 121
DB 69 ALKLVHEHLNIVPHRRGLNLDGFFRYLFS-DUNVSISTDKKVVHDMTAPLSHYFTISHN 127
QY 122 SYLTGNSLSDSDTPIAAALRRGVVVELDLWPD-DKGGMKVTHGNTLTNPVFSQKCVT 180
DB 128 TYLTGNSLSDSDTPIAAALRRGVVVELDLWPD-DKGGMKVTHGNTLTNPVFSQKCVT 187
QY 181 AKNNAFTSEYPCVVTIEDHLTSELQHAAILQILGDALYYPPTDALVEFPSPESL 240
DB 188 SIKEHAFVASEYPIVITLEDHLPDLQAKAAENVTVFGDIL-FTCGAELSEFPSPESL 246
QY 241 KRKIIITKPKPEYACSTQKIAMENRNILVEELEKEDKLEOTTAPLEENHILGENTPS 300
DB 247 KGRIIITKPKPEYACSTQKIAMENRNILVEELEKEDKLEOTTAPLEENHILGENTPS 300
QY 301 LRKEVEVLSQKEMSTPAELNSRPSDLGEATSTRYSKSDGNDNDNPKHFKYARLTIRAK 360
DB 285 WGAETSDLSQK-MTAYSENKDNQECQDEADSHHEPNTOQNAP---EYKHLIAIOAGK 340
QY 361 HAKGTSMEHRLQVDE-SVKRISLESKLEKVPKPEALVKFTQKNILRVYPAANRVNS 419
DB 341 -SKGFTSEW-LTVDPKIKRISLNEEKLINVALNHGKDLIRFTQRLNRIYPKGMVDS 398
QY 420 NFPCTPLANNYGAQVVAQNMGGYKELWQAFGKKGCGGCVLKPQVLLLENLPSPGVFPNP 479
DB 399 NYNPLMGWHAQVVAQNMGGYKELWQAFGKKGCGGCVLKPQVLLLENLPSPGVFPNP 458
QY 480 TSPPRTTLLIKTKVMTTLGWDKAFSKRHFDFLSPDPFFTRVIVGVVPADAKWKTTSVDN 539
DB 459 KRLSVKTLTKVYMGKWHLDKFRTHFDAYSPPDFVYVIGIAGVAADSRVKKTKRAIED 518
QY 540 SWAPHNEDHEPALKCPPELALLRIEVRDHDSDSKDEFGOTCLPIHEVRDGRGCMQYDK 599
DB 519 NWIPIWNEDEFEPPLAVPELALLRIEVRDHDSDSKDEFGOTCLPIHEVRDGRGCMQYDK 578
QY 600 KGNVLKGVLMFLHFOCK 617
DB 579 KGEKPSVKLLMRFEVK 596

RESULT 12

S71170
phosphoinositide-specific phospholipase C (EC 3.1.4.-) - Arabidopsis thaliana
N;Alternate names: phosphodiesterase
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000

plant Physiol. 116, 239-250, 1998
A:Title: Molecular and enzymatic characterization of three phosphoinositide-specific pho
A:Reference number: Z16026; MUID:98111496
A:Accession: T07424
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-565 <KOP>
A:Cross-references: EMBL:X94183; NID:g2853036; PIDN:CAA63893.1; PID:g2853037
A:Experimental source: cv. Desiree
C:Genetics:
A:Gene: PLC2
C:Superfamily: Arabidopsis thaliana 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain Y homology
A:Keywords: phosphoric diester hydrolase
F:107-248/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X homology

Query Match 35.8%; Score 1192.5; DB 2; Length 565;
Best Local Similarity 42.7%; Pred. No. 2.9e-68;
Matches 259; Conservative 98; Mismatches 167; Indels 83; Gaps 14;
QY 21 VGEVFTIYSENER-MSAEGLLKFLHTEQGDVDFTLDDAKQIMERIRKDKWKSFGGLASINS 79
DB 27 IKNLFRYSDSGVQNLHRLFLIDIQEKNASLDNAEALINHGGSQKQ-----K 78
QY 80 DLSKEAFKRYL---MNPDLNGLVHNVVHODMTOPMSHYFTIGHNSYLTGNSLSDSDT 136
DB 79 GLQIDGFFNCLFSDVNPPLDPKLG--IHHDNMAPLSHYIYTGHSYLTGNSLSDSDT 136
QY 137 PIAAALRGVVRVELDLWPD-DKGGMKVTHGNTLTNPVFSQKCVTAIKNNAFTSEYPCV 195
DB 137 PIQALQSRVVRVELDLWPNSDKDDIEVLHGRITLTPAVALLKRLSKEHAFSASEYPVV 196
QY 196 VTIEDHLTSELQHAAILQILGDALYYPPTDALVEFPSPESLKRKIIITKPKPEYL 255
DB 197 ITLEDHLPDLQAKAAENVTVFGDIL-FTCGAELSEFPSPESLKRKIIITKPKPEYL 254
QY 256 EACSTQKIAMENRNILVEELEKEDKLEOTTAPLEENHILGENTPSLRKEVEVLSQKEMST 315
DB 255 QS-----REVKEKDDTKKEAQDDVDE-----EED----- 280
QY 316 PAELNSRPSDLGEATSTRYSKSDGNDNPKHFK-----YARLTIRAKHAKGTSMEHR 370
DB 281 -----DEDEDEDEPKSEKAAASEYKRLIAHAGKGGGLS--DW 318
QY 371 LOVD-ESVKRISLESKLEKVPKPEALVKFTQKNILRVYPAANRVNSNFCPTLANNY 429
DB 319 LRVDLNVKRRSLSPLEKAVDTHSKRIIRFTQONLRIYPKGIRVDSNYPDFVGMWH 378
QY 430 GAQVVAQNMGGYKELWQAFGKKGCGGCVLKPQVLLLENLPSPGVFPNPTS--PRNTTL 487
DB 379 GAQVVAQNMGGYKELWQAFGKKGCGGCVLKPQVLLLENLPSPGVFPNPTS--PRNTTL 437
QY 488 ILKIKVMTTLGWDKAFSKRHFDFLSPDPFFTRVIVGVVPADAKWKTTSVDN 547
DB 438 -LKVTVYMGDGDWDDQDFHFTYSPDFYAKLGTAGVADPEVKKRTKTMDDNIPSWDE 496
QY 548 DHEFALKCPPELALLRIEVRDHDSDSKDEFGOTCLPIHEVRDGRGCMQYDKGNVLKGV 607
DB 497 QFEPTLVPELALLRIKVLVDYNSDKDEFAGOTCLPVAELRQGIKRAVPLDGRKGEKYSV 556
QY 608 LMLHFOCK 614
DB 557 KLLMRFE 563

RESULT 11

T07421
phosphoinositide-specific phospholipase C (EC 3.1.4.-) PLC1 - potato
N;Alternate names: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase
C;Species: Solanum tuberosum (potato)
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
C;Accession: T07421

Result No.	Query			ID	Description
	Score	Match	Length		
1	600	18.0	801	PIPA_DICDI	Q02158 dictyosteli
2	594.5	17.9	695	PID1_BOVIN	P10895 bos taurus
3	594.5	17.9	756	PID1_RAT	P10688 rattus norv
4	577.5	17.4	756	PID1_HUMAN	P51178 homo sapien
5	549.5	16.5	1023	PID4_BOVIN	Q07722 bos taurus
6	536.5	16.1	1175	PID4_HUMAN	Q15147 homo sapien
7	535	16.1	1181	PID2_HUMAN	Q00722 homo sapien
8	522.5	15.7	1175	PID4_RAT	Q9CQW0 rattus norv
9	516.5	15.5	1095	PIPA_DROME	P13217 drosophila
10	506.5	15.2	1234	PIP3_MOUSE	P51432 mus musculu
11	504.5	15.2	1216	PID1_BOVIN	P10894 bos taurus
12	501	15.1	1216	PID1_HUMAN	Q9Nq66 homo sapien
13	499	15.0	1216	PID1_RAT	P10687 rattus norv
14	495	14.9	1234	PIP3_HUMAN	Q01970 homo sapien
15	476	14.3	899	PLC1_SCHPO	P40977 schizosacch
16	464.5	14.0	1312	PIP1_DROME	P23455 drosophila
17	457.5	13.7	1265	PIG2_RAT	P24135 rattus norv
18	448.5	13.5	1252	PIG2_HUMAN	P16885 homo sapien
19	428	12.9	869	PLC1_YEAST	P32383 saccharomyc
20	422.5	12.7	1099	PIG1_CANAL	O13433 candida alb
21	412.5	12.4	1291	PIG1_BOVIN	P08487 bos taurus
22	409.5	12.3	1290	PIG1_RAT	P10686 rattus norv
23	399	12.0	1290	PIG1_HUMAN	P19174 homo sapien
24	134.5	4.0	1679	Y109_YEAST	P40457 saccharomyc
25	132	4.0	722	MFPI1_TOBAC	Q9M7J4 nicotiana t
26	128	3.8	1616	P200_MYCGE	Q49429 mycoplasma
27	125	3.8	771	SKN1_YEAST	P33336 saccharomyc
28	123.5	3.7	2145	CYAA_PODAN	Q01513 podospora a
29	120	3.6	3210	CENF_HUMAN	P45454 homo sapien
30	119	3.6	3068	POLG_PEMVC	Q01500 p genome po
31	116.5	3.5	556	V1E2_AGRV5	P08062 agrobacteri
32	116	3.5	1997	OTOF_HUMAN	Q9HC10 homo sapien
33	115.5	3.5	1603	VIT5_CAEAL	P06125 caenorhabdi

DR Pfam; PF00387; PI-PLC-Y; 1.
 DR PRINTS; PR00360; C2DOMAIN.
 DR PRINTS; PR00390; PHPLIPASE.
 DR PRODOM; PD001202; PI_PLC_Y; 1.
 DR SMART; SM00239; C2; 1.
 DR SMART; SM00148; PLCX; 1.
 DR SMART; SM00149; PLCYC; 1.
 DR PROSITE; PS00018; EF_HAND; 1.
 DR PROSITE; PS50004; C2_DOMAIN_2; 1.
 DR PROSITE; PS50007; PIPLC_X_DOMAIN; 1.
 DR PROSITE; PS50008; PIPLC_Y_DOMAIN; 1.
 KW Hydrolyase; Lipid degradation; Transducer; Calcium-binding;
 KW Phosphorylation.
 FT DOMAIN 322 464 DOMAIN X.
 FT DOMAIN 542 652 DOMAIN Y.
 FT DOMAIN 661 765 C2 DOMAIN.
 FT CA_BIND 490 501 EF_HAND (POTENTIAL).
 FT ACT_SITE 337 337 BY SIMILARITY.
 FT ACT_SITE 382 382 BY SIMILARITY.
 FT MOD_RES 524 524 PHOSPHORYLATION (POTENTIAL).
 FT MOD_RES 531 531 PHOSPHORYLATION (BY CAPK AND CGPK)
 FT (POTENTIAL).
 SQ SEQUENCE 801 AA; 91280 MW; DB4F8C829812DD9 CRC64;
 Query Match 18.0%; Score 600; DB 1; Length 801;
 Best Local Similarity 27.1%; Pred. No. 3.7e-31;
 Matches 167; Conservative 117; Mismatches 249; Indels 84; Gaps 18;
 QY 24 VFTIYS--ENERSARGELKFLHTEQGDVDTLDDAKQIMERIRKDWKSFGLASINSD- 80
 DB 247 VFYKINGNGEWPVIGMDFRIEQSEV-WTEQCRLDKLVHHE-----RLDC 295
 QY 81 LSKEARPKYLM-NPDLNGVLH-NVHQDMTPQMSHVFITGHSYLTGNQSSDSDTFI 138
 DB 296 ISPFNEEFECGBANLAQYPTSTVQDTSKPLSYFINSNHTYLSGHOLGLSTSEMY 355
 QY 139 AALRRGVVRVVELDLPDDKGMKVTGNTLTNPVSFQKCVTAIKNNAFTSPYPCVTI 198
 DB 356 TWTLRQCKVELDVWDGNDGDIIFHGNLTLSQIKFHCETIKARGETSPYPVILSL 415
 QY 199 EDHLTSELQGHAAIEQLIGLDALYYPPTDVALVEFPSPESLKRKIIITKPKKEYLAC 258
 DB 416 EVCHSVPOQIMANHMKFIEMGL-PTPLPEGTKEPLTDLKLYKILLKGHTSHTVSVA 474
 QY 259 STOKLAMENLVLEEKEDKLEQTFAPLEENHILGENTPSLRKEVYLSQKEMSTPAE 318
 DB 475 GNSASSSSQSNITQDNDDD-----GAVDLTEYDE 504
 QY 319 LNSRPSDLGEATSTRYSKSDNDGNPKHFKYARLITIRLAKHAKGT--SMERHLQVDES 376
 DB 505 VDRSASSSSSSFSLSFGSSG-----KKKKITKIKIAPEFEELIYLVSHGFKSGNT 555
 QY 377 VKRI-----SLSEKLEKVEKWPALVKFTQKNILRVYPAANRVNSNFCTLAWNYG 430
 DB 556 TKEIPSYKIHLSVEEKVQQLVQSEPREVVEASQNHLLRVYPRGTFRDSSNDFMPMGWSIG 615
 QY 431 AQMVAAQMGYKELQAQKFKGNGCGVYLPQVLLNLPVGVFNFTSP-----RN 484
 DB 616 CQLAALNQQTSSPFWINDGFMNDGCGGVYLPQVLLNLPVGVFNFTSP-----RN 484
 QY 485 TTLILKIVMTTLGWDAKFSKRFDLFSPPDFTRIVVGVPADEAKKTSVVDNS-WAP 543
 DB 674 SRLI--VNVISARQLPKYTKSTGEVDP--VVTLISVGTHTDQVKETKVIDNNGFNP 728
 QY 544 HWNEDHEFALKCEPALLRIEVRDHDHDDSKDEFGEGTCLPIHEVRDGYRCMQMDYKKNV 603
 DB 729 HWGEFEFPLYNQSLMLIRVDKQVGNHRI-GHCHIRVENIRPGYRILKLNKNFNR 787
 QY 604 LKGVLMLEHFKQCKCTF 620
 DB 788 IPLANLL-----CKFTF 799

RESULT 2
 PIDL_BOVIN
 ID PIDL_BOVIN STANDARD; PRT; 695 AA.
 AC PI0895;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase delta 1
 DE (EC 3.1.4.11) (PLC-delta-1) (Phospholipase C-delta-1) (PLC-III)
 DE (Fragment).
 GN PLCD1.
 OS Bos taurus (Bovine).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovidae; Bovinae; Bos.
 CC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88270495; PubMed=3390863;
 RA Suh P.-G., Ryu S.H., Moon K.H., Suh H.W., Rhee S.G.;
 RT "Cloning and sequence of multiple forms of phospholipase C.";
 RL Cell 54:161-169(1988).
 CC !- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES
 CC DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS
 CC MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE
 CC C ENZYMES.
 CC !- CATALYTIC ACTIVITY: 1-phosphatidyl-1D-myo-inositol 4,5-
 CC bisphosphate + H(2)O -> D-myo-inositol 1,4,5-trisphosphate +
 CC diacylglycerol.
 CC !- COFACTOR: REQUIRES CALCIUM.
 CC !- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS OF
 CC PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
 CC !- SIMILARITY: CONTAINS 1 C2 DOMAIN.
 CC !- SIMILARITY: CONTAINS 1 PH DOMAIN.
 CC !- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
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 CC -----
 CC EMBL; M20638; AAA30710.1; -
 CC PIR; C28821; C28821.
 CC HSSP; PI0688; IMAI.
 CC InterPro; IPR000008; C2.
 CC InterPro; IPR002048; EF-hand.
 CC InterPro; IPR001849; PH.
 CC InterPro; IPR000909; PI_PLC_X.
 CC InterPro; IPR001711; PI_PLC_Y.
 CC Pfam; PF00168; C2; 1.
 CC Pfam; PF00036; ehand; 2.
 CC Pfam; PF00169; PH; 1.
 CC Pfam; PF00388; PI-PLC-X; 1.
 CC Pfam; PF00387; PI-PLC-Y; 1.
 CC ProDom; PD001202; PI_PLC_Y; 1.
 CC SMART; SM00239; C2; 1.
 CC SMART; SM00148; PLCX; 1.
 CC SMART; SM00149; PLCYC; 1.
 CC PROSITE; PS00018; EF_HAND; 2.
 CC PROSITE; PS50003; PH_DOMAIN; 1.
 CC PROSITE; PS50004; C2_DOMAIN_2; 1.
 CC PROSITE; PS50007; PIPLC_X_DOMAIN; 1.
 CC PROSITE; PS50008; PIPLC_Y_DOMAIN; 1.
 KW Hydrolyase; Lipid degradation; Transducer; Calcium-binding; Repeat.
 FT NON_TER 1
 FT DOMAIN 1 69 PH.
 FT CA_BIND 92 103 EF_HAND 1 (POTENTIAL).
 FT CA_BIND 128 139 EF_HAND 2 (POTENTIAL).
 FT DOMAIN 235 379 DOMAIN X.

Sun Jul 28 10:34:37 2002

us-09-828-447-12.rsp

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DR PRINTS; PR00390; PHPLIPASEC.
DR PRODOM; PD001202; PI_PLC_Y; 1.
DR SMART; SM00239; C2; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00148; PLCX; 1.
DR SMART; SM00149; PLCYC; 1.
DR PROSITE; PS00018; EF_HAND; 2.
DR PROSITE; PS00003; PH_DOMAIN; 1.
DR PROSITE; PS00004; C2_DOMAIN; 2.
DR PROSITE; PS00007; PIPLC_X_DOMAIN; 1.
DR PROSITE; PS00008; PIPLC_Y_DOMAIN; 1.
KW Hydrolase; Lipid degradation; Transducer; Calcium-binding; Repeat;
KW 3D-structure.
FT DOMAIN 21 130 PH.
FT CA_BIND 153 164 EF_HAND 1 (POTENTIAL).
FT CA_BIND 189 200 EF_HAND 2 (POTENTIAL).
FT DOMAIN 296 440 DOMAIN X.
FT DOMAIN 492 609 DOMAIN Y.
FT DOMAIN 630 720 C2 DOMAIN.
FT ACT_SITE 311 311
FT ACT_SITE 356 356
SQ SEQUENCE 756 AA; 85962 MW; E33F2313AC81E9F9 CRC64;

Query Match 17.9%; Score 594.5; DB 1; Length 756;
Best Local Similarity 28.7%; Pred. No. 7.7e-31;
Matches 173; Conservative 96; Mismatches 215; Indels 119; Gaps 16;

QY 32 ERMSAEGLLKFLHTQGDVDFTLDDAKQIMERIRKDWKSKFGLASINDLSKEAFKRYLM 91
DB 226 ETLSEVERLVTFHQHOREEAGPALALSRIERYEPS-----ETAKAQRQMTKDFGLMYLL 280

QY 92 NFDLNL--GVILNVHQDTPMASHVFIETGHSYLTGNOLSSDSDTPIAALRGVRVV 149
DB 341 ELDGWDGPNQPEIYHYGFTSKILFCDVLRADYAFKASPPYVLSLENHCSLEQQRV 400

QY 210 AAELIQLGLDALYPPPTDVALVEFSPSLKRIIISTK-----PPK 252
DB 401 MARHLRAILGPIILLDQPLDGVTTSLPSPQLKGLKILLKGLGILLPAGGENGSEATDVS 460

QY 253 EYLEACSTOKLAMENLNVEELEKEKDLQTTFAPLEENHILGENTPSLRKEVEVLSQKE 312
DB 461 DEVERAEMEDAV--RSQVHKPKEDKLL-----VPEL-----492

QY 313 MSTPAELNSRSPDLGEATSTRYSKSDNGDNPKHFKYARLITIRLAKHAKTSMERHLQ 372
DB 493 -----SDM-----IYCKS-----VHFG-----GFSSPGTSGQAFYE 519

QY 373 VDSVKRISISESKLEKVEKPEALVKFTOKNLRVYPAANRVNSNFCPTLAWNYGAQ 432
DB 520 M-----ASFSESRALRLQESNGFVRNVSCLSRIYPAGWRTDSNYPVEMNGGQ 573

QY 433 MVAQNMQGKGKELQWAFKFGKNGCGGYVLKPOYLENLPSGVFPNPTSPRNTLLI-----488
DB 574 IVALNQTPGPEMDVYLGCFQDNGCGGYVLKPAFLRD-----PNTTFNSRALTOGP 624

QY 489 -----LKKVWTTLGDWKAFAKSRHDLSPDPDFTRVIWV--GVPADEAKWKTSVV--DN 539
DB 625 WWRPERLRVRIISQOQLPKV--NKNKNSIVDP-----KVIVETHGVGRDTGSRQTAVITNN 678

QY 540 SWAPHNEDHEFALCPALALLRIEVRDHDSDSKDFEGOTCLPIHEVRDGYRCMOMYDK 599
DB 679 GFNPRMDMEFEFTVTPDLALVRFWVEDYDSSKNDFIGOSTIPWNSLKQGYRHVILLSK 738

QY 600 KGN 602
DB 739 NGD 741
```


Db 69 KTDYLVQDVLFNEHQDPRLNEILFPYDAKRAMQIEMEPDEDLKKQ-GL----- 122
 QY 80 DLSKEAFKYLMPDLNGVLHN--VVHDMTQPMQSHVFTGHNSVLTGNQLSSDSDTP 137
 Db 123 -ISSDGFVRLMSDENAPVFLDRLELYQEMDHLAYFTSSINTYLTGRQFGCKSSVEM 181
 QY 138 IAAALRGVRVVDLWDPDKGMK---VTHGNTLNPVSKFCVTAIRNAFFTEYEPV 194
 Db 182 YRQVLLAGCRVCLDCW-DKGEDQEPITTHGRAMCTDILFKVDVQIAIKETAPVTSEYPV 240
 QY 195 CVTIEDHLTSELQGHAAEILQLGALYPPPTDALVE---FPSPESLKRKIII--- 246
 Db 241 ILSFENHCSKYQKMSKYCEDLFGDLLKQALESHPLEGRPLPSPDLKRILIKKQT 300
 QY 247 -STKPPEYLEACSTOKLAMENRNLVEELEKEDKLEQTTTFAPLEENHILGENTPPSLRKEV 305
 Db 301 TETEVEKQLEALKSMMEAGESAAPVNMLEDNE-----EET 337
 QY 306 EVLSQKEMSTPAEL--NSRSPDLG--EATSTRYSKNDG--NDNPK----- 346
 Db 338 ESAEQEEEAHPYKYKYNELSDADLGHKEATANSVKKASDDLEHNSKKGILVTVEDEQAWM 397
 QY 347 -HFKYARLIT-----IRLAKHAK---GFSMEHRLQVDSVKRISLSESKLEKVE 392
 Db 398 ASKYVCATNIHPYLSLTMNYAOPVKFGFVHAEERNTHYNS-----SFNSVGLGYLK 453
 QY 393 KWPEALVKTQKILNLYVPAANRVNSNFCPTLANNYGAQVMAQNMGGYKELWQAFGR 452
 Db 454 THAIEFVNYNKRMSYRIPKGRVDSNTPYQIFWNSGCMVSLNYQTDLAMQLNQGRF 513
 QY 453 KNGGCGYVLPKYLENLPSGVPENPTSPRNTTLIKIKVMTLW---DKAFSKRHED 509
 Db 514 EYNGSCGYLLKPFMRPRTDPPFSET-PVGVTAATCSQVDSQVIGQFLSDKKIGT--- 568
 QY 510 LFSPPDFTRVIVGVGPAD--EAKWKT-SVVDNSWAPHNEDHEFALK---CPELALLRI 563
 Db 569 -----YVEVDYMGLEPTDIRKEFRVMYMNGLNPNVNEE-SFVERKVLPLDLAVLRI 620
 QY 564 EYRDHDDSKDEFGQTCPLPIHEVRDGYRCMOMYDKGN 602
 Db 621 AV--YDDNNK--LIGQRILPLDLQAGYRHSILRN-EGN 654
 RESULT 6
 PTB4_HUMAN
 ID P1B4_HUMAN STANDARD; PRT: 1175 AA.
 AC Q15147; Q9J0J2; Q9B0W5; Q9B0W6; Q9B0W8;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta 4
 DE (EC 3.1.4.11) (PLC-beta-4) (Phospholipase C-beta-4).
 GN PLCB4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID:9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Retina;
 RX MEDLINE=96079091; PubMed=8530101;
 RA Alvarez R.A., Ghalavini A.J., Xu P., Hardcastle A., Bhattacharya S.,
 Rao P.N., Pettenati M.J., Anderson R.E., Baehr W.;
 RT "cDNA sequence and gene locus of the human retinal phosphoinositide-
 specific phospholipase-C beta 4 (PLCB4).";
 RL Genomics 29:53-61(1995).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
 Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggeley C.L.,
 Bailey J., Barlow K.F., Bates K.N., Bead L.M., Beare D.M.,
 Beasley O.P., Bird C.P., Blakey S.E., Bridgman A.M., Brown A.J.,
 Buck D., Burrill W., Butler A.P., Carder C., Carter N.P.,

RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 Clegg S., Copley V.E., Collier R.E., Connor R., Corby N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhami P., Dunn M.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Gammham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Levasiaho M.H., Leversha M., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConachie L.J., McBay K., McMurray A.A.,
 RA Milne S., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swann M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RL "The DNA sequence and comparative analysis of human chromosome 20.";
 Nature 414:865-871(2001).
 CC -1- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES
 DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS
 CC MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE
 CC C ENZYMES. THIS FORM HAS A ROLE IN RETINA SIGNAL TRANSDUCTION.
 CC -1- CATALYTIC ACTIVITY: 1-phosphatidyl-1D-myo-inositol 4,5-
 CC bisphosphate + H(2)O = D-myo-inositol 1,4,5-trisphosphate +
 CC diacylglycerol.
 CC -1- COFACTOR: REQUIRES CALCIUM.
 CC -1- ALTERNATIVE PRODUCTS: At least 3 isoforms; 1, 2 (shown here) and
 CC 3; are produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN THE RETINA.
 CC -1- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN FOUR DIFFERENT FORMS
 CC OF PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
 CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
 CC -----
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 CC -----
 CC EMBL; AL031652; CAA21068.1; -
 CC EMBL; AL023805; CAC34525.1; -
 CC EMBL; AL023805; CAC34527.1; -
 CC EMBL; AL023805; CAC34528.1; -
 CC EMBL; L41349; AAB02027.1; -
 CC HSSP; P10688; IDJX.
 CC MI: 600810; -
 CC InterPro; IPR000008; C2.
 CC InterPro; IPR001192; PI-PLC.
 CC InterPro; IPR000909; PI-PLC_X.
 CC InterPro; IPR001711; PI-PLC_Y.
 CC Pfam; PF00168; C2; 1.
 CC Pfam; PF00388; PI-PLC-X; 1.
 CC Pfam; PF00387; PI-PLC-Y; 1.
 CC PRINTS; PR00390; PHPLIPASEC.
 CC ProDom; PD001202; PI-PLC_Y; 1.
 CC SMART; SM00239; C2; 1.
 CC SMART; SM00148; PLCXC; 1.
 CC SMART; SM00149; PLCYC; 1.
 CC PROSITE; PS50004; C2_DOMAIN_2; 1.
 CC PROSITE; PS50007; PIPLC_X_DOMAIN; 1.
 CC PROSITE; PS50008; PIPLC_Y_DOMAIN; 1.
 CC Hydrolase; Lipid degradation; transducer; Phosphorylation; Calcium;
 KW Alternative splicing.
 KW DOMAIN 313 463 DOMAIN X.
 FT DOMAIN 565 681 DOMAIN Y.
 FT DOMAIN 688 786 C2 DOMAIN.
 FT ACT_SITE 328 328 BY SIMILARITY.


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FT CONFLICT 1057 1057 A -> V (IN REF. 3).
FT CONFLICT 1067 1067 L -> V (IN REF. 3).
FT CONFLICT 1084 1084 S -> C (IN REF. 3).
SQ SEQUENCE 1175 AA; 134496 MW; 7379C6BB95B8FCE CRC64;

Query Match 15.7%; Score 522.5; DB 1; Length 1175;
Best Local Similarity 28.0%; Pred. No. 6.5e-26;
Matches 180; Conservative 98; Mismatches 243; Indels 105; Gaps 26;

QY 30 ENERMSAEGLLKFLHTQGD-----VDFTLDDAK---QIMERIRKDWK-KSFGLASINSD 80
Db 233 KTDYTLVDOLVSFLNEHQDRPRLNEILFPFYDAKRAQIILEMYPDEELKKGL-----286
QY 81 LSKEAFKRYLMNPDLNGLVH--VVHODMTQPMKSHYFIPTGHSYLTGNLSDDSDTPI 138
Db 287 ISSDGFRLMSDENAPVFLDRLELYQEMDPLAHYFISSHNTYLTGROFGKSSVEMY 346
QY 139 AAALRRGVVVVELDLPDDKGMK---VTHGNTLTNPVSPQKVTALKNNAAFTSEYVPC 195
Db 347 RQVLLAGRCVVELDCW-DGKGEDEQEPITTHGKAMCTDILFKDVIQAIKETAFTSEYVPI 405
QY 196 VTIEDHLSLQGHAAEILQILGDALYPPPTDALVE-----PPSPESLKRKIIISTK-- 249
Db 406 LSFENHCKYQOYQMSKYCEDLFDGLLLKQALSHPLGRLPLSPNDLKRKILIKNKL 465
QY 250 ---PPKEYLEACSTQKLAENRNVLVELEKEDKLEQTTFAPLEENHILGENTPSLRKEYE 306
Db 466 KPEVEKQLEALKSMFAGESAAPASTILEDNE-----EEIE 502
QY 307 VLSQKEMSTPAEL--NSRSPSDLG--BATSTRYSKS-----NGDNDNPKHFKYARLIT--- 355
Db 503 SADQEEEAHPYKFGNELSADDFSHKEAVANSVKGLVTVEDDQAMWASVKYVGVATNIH 562
QY 356 -----LRLAKHAK---GTSMEHRLQVDSVKRISLSKLEKVEKWEALVKETQKN 405
Db 563 PYLSTMIYAQPQKFGFHVAAEERNIHNMS-----SFNEVSLGLYKLTHTAIEFVNYNKRO 618
QY 406 ILRYPAANRVSNFCPTLAWNYGAQMAQNMQGYGKELWQAFKFGKGGCGYVVKQ 465
Db 619 MSRIYKGGVRVDSNNYMPQIFWAGQMVSLNYQTPDLAQLNOGFEYVNGSCYLLKLPD 678
QY 466 YLENLPSGVFPNPTSPRNTLLIKTKVMTLGN-----DKAFSKRHPDLSPDPDFRTRIV 522
Db 679 FMRRPRTDFPFSET-PVDGVIAATCSQVVISGFLSKDKIGT-----YVEVDM 726
QY 523 VGVPAD--EAKMKT-SVWDNSWAPHNNEDEHFAK--CPELALLRIEVRDHDSDSKDEF 576
Db 727 YGLPTDTRKEFTRMVNNGLNPNVINEE-SFVFRKVIPLDLAVLRIAV--YDDNNK--L 781
QY 577 EGOTCLPIHEVRDGYRCMQMYKKGN 602
Db 782 IGQRILPLDGLQAGYRHSILRN-EGN 806

RESULT 9
PIPA_DROME STANDARD; PRT; 1095 AA.
ID PIPA_DROME
AC P13217;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase
DE (EC 3.1.4.11) (Phosphoinositide-specific phospholipase C).
GN NORPA.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88311074; PubMed=2457447;
```

```
RA Bloomquist B.T., Shortridge R.D., Schneuwly S., Perdew M.H.,
RA Montell C., Steeller H., Rubin G., Pak W.D.;
RT *Isolation of a putative phospholipase C gene of Drosophila, norPA,
RT and its role in phototransduction.*;
RL Cell 54:723-733(1988).
CC !- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES
CC DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS
CC MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE
CC C ENZYMES. NORPA IS INVOLVED IN PHOTOTRANSDUCTION.
CC !- CATALYTIC ACTIVITY: 1-phosphatidyl-1D-myo-inositol 4,5-
CC bisphosphate + H(2)O = D-myo-inositol 1,4,5-trisphosphate +
CC diacylglycerol.
CC !- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS OF
CC PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
CC !- SIMILARITY: CONTAINS 1 C2 DOMAIN.
CC
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CC
CC EMBL: J03138; AAA28724.1; -.
CC PIR: A31225; A31225.
CC HSP: P10888; IQAS.
CC FlyBase: FBgn0004625; norPA.
CC InterPro: IPR000008; C2.
CC InterPro: IPR001192; PI-PLC.
CC InterPro: IPR000909; PI-PLC_X.
CC InterPro: IPR001711; PI-PLC_Y.
CC Pfam: PF00168; C2; 1.
CC Pfam: PF00388; PI-PLC-X; 1.
CC Pfam: PF00387; PI-PLC-Y; 1.
CC PRINTS: PR00390; PHPLIPASEC.
CC ProDom: PD001202; PI-PLC_Y; 1.
CC SMART: SM00239; C2; 1.
CC SMART: SM00148; PLCX; 1.
CC SMART: SM00149; PLCYC; 1.
CC PROSITE: PS50004; C2_DOMAIN_2; 1.
CC PROSITE: PS50007; PIPLC_X_DOMAIN; 1.
CC PROSITE: PS50008; PIPLC_Y_DOMAIN; 1.
CC KW Hydrolase; Lipid degradation; Vision; Transducer.
CC FT DOMAIN 320 469 DOMAIN_X.
CC FT DOMAIN 550 666 DOMAIN_Y.
CC FT DOMAIN 673 771 C2 DOMAIN.
CC FT ACT_SITE 334 381 BY SIMILARITY.
CC FT ACT_SITE 381 381 BY SIMILARITY.
CC SQ SEQUENCE 1095 AA; 124822 MW; 2D945EF0ACBE69B3 CRC64;
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Query Match 15.5%; Score 516.5; DB 1; Length 1095;
Best Local Similarity 28.0%; Pred. No. 1.4e-25;
Matches 178; Conservative 113; Mismatches 250; Indels 95; Gaps 27;
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QY 12 PKGDEQDLVGEVETIYSENER--MSAEGLLKFLHTQGD-----VDFTLDDAKQIMERI 64
Db 224 PRNDIE-----ELFTSITKQKDFISLEQFIQFMNDKQDRPMNEILYPLYEKRCTEII 278
QY 65 R-----KDWKKSFGLASINSLSKAFKRYLMNPDLNGLVHNV--HQDMTPQMSHYFIF 117
Db 279 NDYELDEKKK-----NVQMSLDGFKRYLMSDENAPVFLDRDLDFYEMDQPLAHYIN 331
QY 118 TGHNSYLTGNLSDDSDTPTAAALRGVRVVELDMLPDDKGMK-----VTHGNTLTNPVS 174
Db 332 SSHNTYLSGRIGKGSVSEMYRQTLLAGRCVVELDCW--NGKGEDEPIVTHGAYCTEIL 390
QY 175 FOKCVTAIKNNAAFTSEYVPCVTIEDHLSLQGHAAEILQILGDALYPPPTDALVE-- 233
Db 391 FKDCIQAIDACAFVSSEYVILSFENHCNRAQQYKLAICYDDDFDGLLLKEPLDRLDP 450
QY 234 ---FPSPESLKRKIIISTKPPKEYLEACSTQKLAENRNVLVELEKEDKLEQTTFAPLEE 290
```


Db	451	GLPLPPCKLKKKILIKNKRKPEVE-----KVELE-LWLKELKTDDEEDA-----	498
Qy	291	NHILGENTPSLRKEVEVLSQKEMSTPAELNRSRSDLG-----EATSTRYSKSDGNDNP	345
Db	499	-----SACKPEAAAAAPAPAAAAAAGGAEGGGAAEAAAAAANSYSGSTT-NVHP	548
Qy	346	---KHFKYARLITIRLAKHAGTSMHRL-QVDESVKRISLESKLEKVKVEKPEALVKP	401
Db	549	WLSSMVNTAQPITKFGDFKATEKNIAHNMSFAESAGMNYLKQSSID-----FVNY	599
Qy	402	TOKNLTIRVYPAANRVNSNFCPTLAWNYGAQVNAQNMGGYCKELWAFQKMGNGCGYV	461
Db	600	KRQMSRIYPKGTGRADSSNIPQVFNWAGCQMVSNFSSDLPQNLGCKEYNGCGYL	659
Qy	462	LKQYLLLENLPSGVFPNFTSPRNTTLIKIKVMTTLGWDKAFSRHEDLFSPPDPFFTRVI	521
Db	660	LKPDPMRADKDFDF-ADAPVDGVIAAOCVKVIAG--QFLSDKKVGYTVEVDMF----	712
Qy	522	VGVPADEAK--WKTSVV-DNSWAPHNEDHEFALK---CPELALLRIEVRDHDSDKDE	575
Db	713	--GLPSTVVKKEFRTRLVANGLNLYNED-PFVERKVVLPDLAVLRFV--YEESGK--	765
Qy	576	PEGQCLPIHEVRDGYRCMOMYDKKGNVKGVLMLF 611	
Db	766	ILQRIPLDGLQAGYRHVSL-RTEANFMSLPMLF 800	
RESULT 10			
PIP3_MOUSE			
Id	PIP3_MOUSE	STANDARD; PRT; 1234 AA.	
Ac	P51432.		
Dt	01-OCT-1996	(Rel. 34, Created)	
Dt	01-OCT-1996	(Rel. 34, Last sequence update)	
Dt	16-OCT-2001	(Rel. 40, Last annotation update)	
De	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta 3		
De	(EC 3.1.4.11) (PLC-beta-3) (Phospholipase C-beta-3).		
Gn	PLCB3.		
Os	Mus musculus (Mouse).		
Oc	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
Oc	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
Ox	NCBI_TaxID=10090;		
Rn	[1]		
Rp	SEQUENCE FROM N.A., AND SUBCELLULAR LOCATION.		
Rc	STRAIN=BAIB/C; TISSUE=Kidney;		
Rx	MEDLINE=98382438; PubMed=9714794;		
Ra	Wang S., Zhou Y., Lukinius A., Oberg K., Skogseid B., Gobl A.;		
Rt	"Molecular cloning and characterization of a cDNA encoding mouse		
Rt	phospholipase C-beta3."		
Rl	Biochim. Biophys. Acta 1393:173-178(1998).		
Cc	-!- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES		
Cc	DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS		
Cc	MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE		
Cc	C ENZYMES.		
Cc	-!- CATALYTIC ACTIVITY: 1-phosphatidyl-D-myo-inositol 4,5-		
Cc	bisphosphate + H(2)O = D-myo-inositol 1,4,5-trisphosphate +		
Cc	diacylglycerol.		
Cc	-!- COFACTOR: REQUIRES CALCIUM (BY SIMILARITY).		
Cc	-!- SUBCELLULAR LOCATION: Nuclear.		
Cc	-!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN KIDNEY, SKELETAL MUSCLE,		
Cc	LIVER, LUNG, HEART AND BRAIN.		
Cc	-!- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS		
Cc	OF PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.		
Cc	-!- SIMILARITY: CONTAINS 1 C2 DOMAIN.		
Cc	-----		
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Cc	the European Bioinformatics Institute. There are no restrictions on its		
Cc	use by non-profit institutions as long as its content is in no way		
Cc	modified and this statement is not removed. Usage by and for commercial		
Cc	entities requires a license agreement (See http://www.isb-sib.ch/announce/		
Cc	or send an email to license@isb-sib.ch).		
Cc	-----		

DR	EMBL; U43144; AAA85199.1; -.		
DR	HSSP; P10688; 1QAS.		
DR	MGD; MGI:104778; Plcb3.		
DR	InterPro; IPR000008; C2.		
DR	InterPro; IPR001192; PI-PLC_X.		
DR	InterPro; IPR000909; PI-PLC_X.		
DR	InterPro; IPR001711; PI-PLC_Y.		
DR	Pfam; PF00168; C2; 1.		
DR	Pfam; PF00388; PI-PLC-X; 1.		
DR	Pfam; PF00387; PI-PLC-Y; 1.		
DR	PRINTS; PR00390; PHPLIPASEC.		
DR	ProDom; PD001202; PI-PLC_Y; 1.		
DR	SMART; SM00239; C2; 1.		
DR	SMART; SM00148; PLCXc; 1.		
DR	SMART; SM00149; PLCXc; 1.		
DR	PROSITE; PS50004; C2_DOMAIN_2; 1.		
DR	PROSITE; PS50007; PIPLC_X_DOMAIN; 1.		
DR	PROSITE; PS50008; PIPLC_Y_DOMAIN; 1.		
KW	Hydrolase; Lipid degradation; Transducer; Calcium; Nuclear protein.		
FT	DOMAIN 318 468 DOMAIN X.		
FT	DOMAIN 591 707 DOMAIN Y.		
FT	DOMAIN 714 811 C2 DOMAIN.		
FT	ACT_SITE 322 322 BY SIMILARITY.		
FT	ACT_SITE 379 379 BY SIMILARITY.		
SQ	SEQUENCE 1234 AA; 139491 MW; 861955DDHB2CC7C255 CRC64;		
Query Match 15.2%; Score 506.5; DB 1; Length 1234;			
Best Local Similarity 27.4%; Pred. No. 7.5e-25;			
Matches 174; Conservative 102; Mismatches 239; Indels 119; Gaps 24;			
Qy	34	MSAEGLLKFLHTEQGDVDF-----DDAKOIMERTKDKWKSFGLA 75	
Db	241	LTLEQLMDFINQKQDRPRLNEVLPPLRSQARLLIEKYETNKQFLER-----	288
Qy	76	SINDLSKEAFKRYLMPDLNGVLHV-----VHODMTPKSHYFTFGHNSYLTGNOLSSD 132	
Db	289	---DQNSMEGFSRYLGEE-NGILPLEALDLSMDMTQPLSAYFINSHNYLTAGQLAGP 344	
Qy	133	SSDPTIAAALRRGVVVVELDLW-----PDRGGMKVTGNTLTNPVSQKCVTAIKNNAF 188	
Db	345	SSVEMYQALLNGRCVELDWKGRPEEE--PFITHGTMTTEVPLRDVLEAIAEAAFK 402	
Qy	189	TSEYPVCVTIEDHLTS-ELQGHAAEILEILGALYPP-----TTDALVEFPSPESLKRK 243	
Db	403	TSPYVILSFENHVDSAKQAQAKAAYCYSIFGDALLDPLDKYPLSAGIPPLSPQDLAMGR 462	
Qy	244	IIISTKP---PKEYLEACSTQKLAENRNLVEELEKEDKLEQTFAPLEENHILG----E 296	
Db	463	ILVANKKRRHSTGVDPSSVKKRPLEQSN-----SALSSESAATEPSSPOLGSPSSD 514	
Qy	297	NTPSLRKEVEVLSQK-----EMSTPAELNRSRPS-----DLGEATSTRYS 336	
Db	515	SCPGLSNGEEVGLKTSLEPQKSLGEESLSREPNVMPDRDRDEDEDEDEETTPPKP 574	
Qy	337	KSNDGNPNKHFYARLIT-IRLAKHAKGSMHRLQVDSVKRISLESKLEKVKVEKWP 395	
Db	575	TTDEGTASSEVNAATEMSTLVNVEPVKFSFEASRRKRCFEMSSFEVETKAMEQLTKSP 634	
Qy	396	EALVKFTQKNLTIRVYPAANRVNSNFCPTLAWNYGAQVNAQNMGGYCKELWAFQKMGK 455	
Db	635	MEFVEYNKQLSRYPKGTGRVDSNNYMPQLFWNVGCOLVALNFQTLDLPMQLNAGVFEYN 694	
Qy	456	GGCGYVLAPQVLLLENLPSGVFPNFTSPRNTLI-----LTKVMTTLGWDKAFSKRH 507	
Db	695	GRSGYLLKPEFMRPRDKSDFP-----TEVIVDGVIVANALRVKVIS----GQFLSDKK 743	
Qy	508	FDLSPDPDFTRVIVGVVPAD-EAKWKTSSVVD-NSWAPHNED-HEF-ALKCPALALLRI 563	
Db	744	VGIVVEVDMF-----GLPVDTRRKRTIRTSQGSFNPVWDEEFDKPKVPLPLASURI 797	
Qy	564	EVROHDDSDSKDFEQTCPLPIHEVRDGYR--CMQ 595	

798 AAFEEG----GKFGHRLPVSAIRSGYHYVCLR 827

Db 1216 AA; 138714 MW; BEF809177F1B7ABB CRC64;

Query Match 15.2%; Score 504.5; DB 1; Length 1216;
Best Local Similarity 26.3%; Pred. NO. 9.9e-25;
Matches 179; Conservative 111; Mismatches 263; Indels 127; Gaps 25;

2 CSIAACRSGTPKGDPEQDLVGEVFTIYSEN-----ERMSAEGLLKF 42
192 CSLPSSRNDSS---IPOEDFTPEVIRVFLNNLCRPEIDNIFSEFGAKSKPYLTVDMMDF 248
43 LHTQGD-----VDFTLDDAKQIMERIKDWKSGFGLASINDSLKEAFKRYLMPDING 97
249 INKORDPLNEILYPLKQEOVQLTEK-YEPNNSLAK-KGOISVDGFMRYLSEEN-NG 305
98 VLHNV---VHDMQPMQSHYFIFGTGNSYLTGNLSDDSDTPIAALRRGVVYVLELDLW 154
306 VVSEPKDLINEDMSQPLSHYFINSHTYITAGQLAGNSSVEMYRQVLLSGRCVELDCW 365
155 PDDKGMK-----VTHGNTLTPVSVFQCVTAIKNNAFFTSEYPCVCTIEDHLTS-ELQG 208
366 ---KGTAEPEVITHGFTMTTEISFKEVIEAIEACAFKSPFILLSPFNHVDSPKQQA 422
209 HAAEILQILGALYYP-----TTDALVEFPSPESLAKKIIISTKPKP-EYLEACSTQKL 263
423 KMAEYCRILFGDALLMEPLDKYPLESGVPLPSPMDLMYKILVKNKKSHKSSGSGKKL 482
264 AMENRNLVELEKEDKLEOTTEAPLEENHILGENTPSPURKEVEVLSKEMSTP-----AEL 319
483 SEQASTYSD-----SSSVFEP-----SSPGAGEADT 509
320 NSRSPDLGENTSTRYKSDNGDNPKHFKYARLITIRLAKHAKGTSMERHLRQVDESVR 379
510 ESDDDDDDCKCKSDMDGTAGSEAMATEMSNL--VNYIOPVAFESFEISKRRSFEM 567
380 ISLESKLEKVKWKEPEALVKFTQKNILRVPAANRVSSNFCPTLAWNYGAQVQNM 439
568 SSFVETKLEQLTKSPVEFVEYKMKLSRIYKPKTRVDSNTPQGLFWNACQWALNFQ 627
440 GYKELMQATGKFKNGCGGVLLKPOYL-----LENLPSGVFPFNP7SPRNTTIL 489
628 TVDLAMQINMGMYEYNGSKYRLKPEMRPKDHPFTEGIVDGVAN-----TSLV 680
490 KIKVMTTLGMDKAFSKRHFDFLSPDPFTRVIVGVPADEA---KWKTSVVDNSWAPHW 545
681 KLIISQFLSDKKVGYVEVDMF-----GLPVDTRRKAFTKTS-OGNAVPIW 727
546 NEDHEFALK--CPELALLRIEVRDHDSDSKDEFGOTCLPIHEVRDGYRCMOMYDKKNV 603
728 EEEPIVFKKVVPLSLACLRIAV--YEEGK--FIGHRLFPVQAIRPGYHYVCLRNOP 783

604 LKGVLMFLHFCKCTFQDT 623
784 LM-LPALFYIEVKDYVDPDT 802

RESULT 12
PIBL_HUMAN
ID PIBL_HUMAN STANDARD; PRT; 1216 AA.
AC Q9NQ66; Q9NQ65; Q9NQ99; Q9NTH4; O60325; Q9H4H2; Q9BQW2; Q9UJF6;
AC Q9UM26;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta 1
DE (EC 3.1.4.11) (PLC-beta-1) (Phospholipase C-beta-1) (PLC-154).
CN PLCB1 OR KIAA0581.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N. A. (ISOFORMS A AND B).

Db 798 AAFEEG----GKFGHRLPVSAIRSGYHYVCLR 827

RESULT 11
PIBL_BOVIN
ID PIBL_BOVIN STANDARD; PRT; 1216 AA.
AC P10894;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta 1
DE (EC 3.1.4.11) (PLC-beta-1) (Phospholipase C-beta-1) (PLC-154).
CN PLCB1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N. A., AND PARTIAL SEQUENCE.
RX MEDLINE=88270496; PubMed=2455601;
RA Katon M., Kriz R.W., Totty N., Philip R., Meldrum E., Aldape R.A.,
RA Knopf J.L., Parker P.J.;
RT "determination of the primary structure of PLC-154 demonstrates
diversity of phosphoinositide-specific phospholipase C activities.";
RL Cell 54:171-177(1988).
CC -!- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES
DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS
MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE
C ENZYMES.
CC -!- CATALYTIC ACTIVITY: 1-phosphatidyl-1D-myo-inositol 4,5-
bisphosphate + H(2)O = D-myo-inositol 1,4,5-trisphosphate +
diacylglycerol.
CC -!- COFACTOR: REQUIRES CALCIUM.
CC -!- MISCELLANEOUS: THE RECEPTOR-MEDIATED ACTIVATION OF PLC-BETA 1 IS
MEDIATED BY TWO G-PROTEIN ALPHA SUBUNITS, ALPHA-O AND ALPHA-11.
CC -!- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS
OF PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
CC -!- SIMILARITY: CONTAINS 1 C2 DOMAIN.
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the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
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or send an email to license@isb-sib.ch).

EMBL; J03137; AAA30702.1;
PIR; A28822; A28822.
HSSP; P10688; IDJX.
InterPro; IPR000008; C2.
InterPro; IPR001192; PI_PLC.
InterPro; IPR000909; PI_PLC_X.
InterPro; IPR001711; PI_PLC_Y.
Pfam; PF00168; C2; 1.
Pfam; PF00388; PI-PLC-X; 1.
Pfam; PF00387; PI-PLC-Y; 1.
PRINTS; PR00390; PHPLIPASEC.
ProDom; PD001202; PI_PLC_Y; 1.
SMART; SM00239; C2; 1.
SMART; SM00148; PLCYC; 1.
SMART; SM00149; PLCYC; 1.
PROSITE; PS50004; C2_DOMAIN_2; 1.
PROSITE; PS50007; PIPLC_X_DOMAIN; 1.
PROSITE; PS50008; PIPLC_Y_DOMAIN; 1.
KW Hydrolase; Lipid degradation; Transducer; Phosphorylation; Calcium.
FT DOMAIN 316 467
FT DOMAIN X.
FT DOMAIN Y.
FT DOMAIN 540 656
FT DOMAIN 663 761
FT DOMAIN 331 331
FT ACT_SITE 378 378
FT ACT_SITE 378 378
FT MOD_RES 887
FT MOD_RES 887


```
CC OF PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
CC -!- SIMILARITY: CONTAINS 1 C2 DOMAIN
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstat
CC the European Bioinformatics Institute. There are no restrictions on t
CC use by non-profit institutions as long as its content is in no way m
CC modified and this statement is not removed. Usage by and for commo
CC entities requires a license agreement (See http://www.isb-sib.ch/anno
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AJ278313; CAB98142.1; -
CC EMBL; AJ278314; CAB98143.1; -
CC EMBL; AY004175; AAF86613.1; -
CC EMBL; AL031683; CAC16181.1; -
CC EMBL; AL031683; CAC34366.1; -
CC EMBL; AL050315; CAB56498.1; -
CC EMBL; AL049632; CAB46663.1; -
CC EMBL; AL137267; CAB70666.1; -
CC EMBL; AB011153; BAA25507.1; -
CC HSSP; P10688; IQAS
CC InterPro; IPR000008; C2.
CC InterPro; IPR001192; PI_PLC.
CC InterPro; IPR000909; PI_PLC_X.
CC InterPro; IPR001711; PI_PLC_Y.
CC Pfam; PF00168; C2; 1.
CC PRINTS; PR00390; PHPLIPASEC.
CC ProDom; PD001202; PI_PLC_Y; 1.
CC SMART; SM00239; C2; 1.
CC SMART; SM00148; PICYC; 1.
CC SMART; SM00148; PICYC; 1.
CC PROSITE; PSS0004; C2_DOMAIN_2; 1.
CC PROSITE; PSS0007; PIPLC_X_DOMAIN; 1.
CC PROSITE; PSS0008; PIPLC_Y_DOMAIN; 1.
CC Hydrolase; Lipid degradation; Transducer; Phosphorylation; Calcium;
KW Alternative splicing.
FT DOMAIN 316 467 DOMAIN X.
FT FT 540 656 DOMAIN Y.
FT FT 663 761 C2 DOMAIN.
FT ACT_SITE 331 331 BY SIMILARITY.
FT ACT_SITE 378 378 BY SIMILARITY.
FT MOD_RES 887 887 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
FT VARSPLIC 1142 1216 LQVELEQYQDKRKLPLETFEVPQAMKGISDSNHGSA
FT SSSLSEDPGVNKHPTSSSELGDGPKEFDIPL -> GEG
FT B).
FT MAGAQPQVHAQLKPVCVSDLSKKGPKFKVQDDD -> MGS
FT LOGIATIKILLRIISDALIRKETDLKS (IN REF. 2).
FT L -> M (IN REF. 2).
FT P -> L (IN REF. 2).
FT L -> F (IN REF. 2).
FT P -> L (IN REF. 2).
FT L -> P (IN REF. 2).
FT P -> T (IN REF. 2).
FT Q -> R (IN REF. 2).
FT V -> A (IN REF. 2).
FT K -> R (IN REF. 2).
FT E -> K (IN REF. 2).
FT P -> S (IN REF. 1; CAB98143).
FT SEQUENCE 1216 AA; 138566 MW; 6F4263DIA50C6FD1 CRC64;

Query Match 15.1%; Score 501; DB 1; Length 1216;
Best Local Similarity 26.1%; Pred. No. 1,7e-24;
Matches 175; Conservative 110; Mismatches 241; Indels 144; Gaps 2

2 CSIIACRSRGTPKGDPQDLVGVEVFITYSN-----ERMSEAELLKF 42
||| : : : : ||| : : : |
192 CSLSPSRNDS---IPQEDTPEYRVFLNNLCRPREDIFSEFGAKSKPVLTVDQMDF 248
||| : : : : ||| : : : |

43 LHTEQQD-----VDFTLDKAQIMERIRKDWKSKFGLASINDLSKFAFRKYLMPDLNG 97
: : | : : : : | : : : : | : : | : : | : : | : : |
249 INLKQRDPLNETLYPLQAQEQOVLIBEYEPNNSLR-KGQISVDGFMYLSGEE-NG 305
```

```

QY 98 VLHNV---VHQDTPQM$H$YFIFTGHSNYLTGNOLSSDSDTPTAAALRRGVVVVELDW 154
Db 11: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
306 VVSEPKLIDNEDMSOPLSHYFINSHTYLTAGLACN$SVEMYRQVLSJGCRGVVELDCW 365
QY 155 PDRKGKMK----VTHGNTLVNPVSQKCVTAIKNNAFFTSEYXVCVTIEDHLTS--ELQG 208
Db 11: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
366 ---KGRTAEEPVTTHGFTTTEISFKEVTEALAECAFKTSPFILLSPENHVDPKQQA 422
QY 209 HAAETLEQLGDALYPP---ITDALVEPSPESLKRKIIISTKPKPKEYLEACSTQKLA 264
Db 11: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
423 KMAEYCRLIIFGDALLMEPLKEYPLESGVPLSPMDLMIYLVKNK-----467
QY 265 MENRLVELEKEDKLEQTTFAPLEENHIIGENTPSLRKEVEVLSOKEMSTPAELNSR-'S' 323
Db 11: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
468 -----KSKHSKSESGRKK-----LSEQASNTYSDSSMFE 498
QY 324 PSDLGEATSTRYK$K$NDGNDNPKHFY-----ARLIT-----IRLAKHAKGT$M$HR 370
Db 11: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
499 PSSPGEADTESDDDDDDDDCKKSSMDGETAGSEAMATEMSNLVNYIQPVKPF$PEIS 558
QY 371 LOVDESVKRISLS$ESKLEKVV$KWPALYKFTQKNILRVYPAANRVNSNFCPTLAWNYG 430
Db 11: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
559 KRNK$FEMS$FVETLGLQ$LT$KSPVEFY$NKMOL$RIYPKRGTRVSDSNM$PQL$FNAG 618
QY 431 AQMYAONMOGYGKELMAQ$FKGNGCGCYVLKPOVL-----LENLPSGV$P$NPT 480
Db 11: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
619 COMVALNFQTM$LAWQINNGW$Y$NGK$GYRLKPF$MRRPKDHPDFTTEGIVDGVAN-- 676
QY 481 SPRNTLLIKVWTLTGW$DKAF$KRHFDL$P$P$DFTTRVIVGV$PADEA----KWKTSV 536
Db 11: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
677 ----T$VKLIISGQ$PL$DKKVGTV$EVD$M$-----GLPVDTRRKA$FKT$TS- 718
QY 537 VDN$WAPHNNEOHE$FALK--CPEALLRLEV$RDHDD$K$DFEGTCLPIHEVRDGYRCM 594
Db 11: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
719 QGN$VNPVWE$EPI$VFKV$VLEP$TLACLR$V--VEEGK--FIGHRLIPVQAIRPGYHYI 774
QY 595 QMYD$K$KNYLV 604
Db 11: : : : :
775 CLRNERNOPL 784

```

RESULT 13

PUBL_RAT	STANDARD	PRT	1216 AA.
AC	P10687;		
ID	P10687		
01-JUL-1989	(Rel. 11, Created)		
01-JUL-1989	(Rel. 11, Last sequence update)		
16-OCT-2001	(Rel. 40, Last annotation update)		
DE	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta 1		
DE	(EC 3.1.4.11) (PLC-beta-1) (phospholipase C-beta-1) (PLC-154) (PLCB1).		
OS	Rattus norvegicus (Rat).		
OC	Rattus norvegicus (Rat).		
OC	Karyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
NCBI_TaxID	10116;		
[1]			
SEQUENCE FROM N.A.			
MEDLINE	=8270495; PubMed=3390863;		
Suh P.-G., Ryu S.H., Moon K.H., Suh H.W., Rhee S.G.;			
"Cloning and sequence of multiple forms of phospholipase C.,"			
Cell 54:161-169(1988).			
-1- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES			
DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS			
MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE			
C ENZYMES.			
-1- CATALYTIC ACTIVITY: 1-phosphatidyl-1D-myo-inositol 4,5-			
bisphosphate + H(2)O = D-myo-inositol 1,4,5-trisphosphate +			
diacylglycerol.			
-1- COFACTOR: REQUIRES CALCIUM.			
-1- MISCELLANEOUS: THE RECEPTOR-MEDIATED ACTIVATION OF PLC-BETA 1 IS			
MEDIATED BY TWO G-PROTEIN ALPHA SUBUNITS, ALPHA-Q AND ALPHA-11.			
-1- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS			

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CC      OF PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
CC      -!- SIMILARITY: CONTAINS 1 C2 DOMAIN.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announcement/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; M20636; AAA41885.1; -.
DR      PIR; A28821; A28821.
DR      HSSP; P10688; 1DJX.
DR      InterPro; IPR000008; C2.
DR      InterPro; IPR001192; PI_PLC.
DR      InterPro; IPR000909; PI_PLC_X.
DR      InterPro; IPR001711; PI_PLC_Y.
DR      Pfam; PF00168; C2; 1.
DR      Pfam; PF00388; PI-PLC-X; 1.
DR      Pfam; PF00387; PI-PLC-Y; 1.
DR      PRINTS; PR00390; PHPLIPASEC.
DR      ProDom; PD001202; PI_PLC_Y; 1.
DR      SMART; SM00239; C2; 1.
DR      SMART; SM00148; PLCXC; 1.
DR      SMART; SM00149; PLCYC; 1.
DR      PROSITE; PS50004; C2_DOMAIN_2; 1.
DR      PROSITE; PS50007; PIPIC_X_DOMAIN; 1.
DR      PROSITE; PS50008; PIPIC_Y_DOMAIN; 1.
KW      Hydrolase; Lipid degradation; Transducer; Phosphorylation; Calcium.
FT      DOMAIN 316 467
FT      DOMAIN 540 656
FT      DOMAIN 663 761
FT      ACT_SITE 331 331
FT      ACT_SITE 378 378
FT      MOD_RES 887 887
SQ      SEQUENCE 1216 AA; 138344 MW; 92F23691781F788E CRC64;

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Query Match 15.0%; Score 499; DB 1; Length 1216;

Best Local Similarity 26.0%; Pred. No. 2.2e-24;
Matches 172: Conservative 110; Microhetero-

matches 172; Conservative 110; Mismatches 253; Indels 126; Gaps 24;

[illegible]

QY 2 CSIAACRSGTPKGDPEQDLVGEVFTIYSEN-----ERMSAEGLLKF 42

[illegible]

Db 192 CSLPSSRNDSP--IPQEDFTPDVYRVFLNNLCPRPEIDNIFSEFGAKSKPYITVDDMMDF 248

----- CARRISOT IN BIDNIT SET CARKNF ILI V DQNMDF 248

QY 43 LHTEQD-----VDFTLDDAKOIMERIRKDWKKSFGI.ASTNSDI.SKEAFBKVI MNDPVC 07

VFIEDDARQIMERTKRDWKA SFGLASINSDLSKEAFRKYLMPDLNG 97

249 TNT.KORDDPRI.NE.TI.VBBI.KOE.FAVI.VT.TE.V - VETENICOT.S.VF

25 INKQRDPRLNETLTPPLKQEQVQVLTIEK-YEPNSSLAK-KGQMSVDGFMRYLSGEE-NG 305

09 VET TYPE - **VETERINARY SERVICES**

98 VLHN - - - VHQMTPQPM SHYFIFTGHNSYLTGNQLSSDSDTPIAAALRRGVRVVELDLW 154

[illegible]

db 306 VVSPEKLDLNEDMSQPLSHYFINSSHNTYLTAGOLAGNSSVEMYRQV.I.SGCRVET.DCW 365

..... Q . E N T I T Y S U B J A C T + E T H O G E A R N S S V E M I K Q V L F S G C K C V E L D C W 365

QY 155 PDDKGGMK-----VTHGNTLTNPVSEOKCVTATKNNAEFTSEYDVCVTYEDHTEC-----EYCC 360

VIMONILIN FVSFQACVIAIKNNAFFTSEYPVCVTIEDHLTS-ELQG 208

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Db 423 KMAEYCR LIFGDALLMEPLEKYPLESGVPLSPMDL MYKILVKNKKSHKSSGSGKKKI. 482

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QY 264 AMENRNLVEELEKEDKLEOTTFAPLEENHTI.GENTPSI.RKEVEVI SOKEVMTD-----AYEY 310

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483 SEASNTYSD-----SSSVFPP-----
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[illegible]

510 ESDDDDDDDDCKKSSMDEGTAGSEAMATEMSNL--VNYIQPVKFESFETSKRNRKSFEM 567

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1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1

[illegible]

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568 SSFVETKLEQLTKSPVEFVEYNKMLSRYYPKGTRVDSNYPQLPWNAGCQWALNFQ 621

QY 440 GYGKELWQAFKFKNGCGGYLKKPOYL-----LENLPQGVFNFTSPRNTLLIL 489

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QY 546 NEDHEFALK--CPALALRIEVRDHDHDDKDFEGQTCLPTHEVRDGVRCMQMWDKKNV 603

DB 728 EEEPIVFKKVVPLSLACLRITAA--YEEGKK--FIGHRLPQVAIRPGYHYICLRNERNQP 783

QY 604 L 604

DB 784 L 784

RESULT 14

ID PIP3_HUMAN STANDARD; PRT; 1234 AA.

AC Q01970;

DT 01-JUL-1993 (Rel. 26, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta 3

DE (BC 3.1.4.11) (PLC-beta-3) (Phospholipase C-beta-3).

GN PLCB3.

OS Homo sapiens (Human).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OC NCBI_TaxID=9606;

RN [1]

RX MEDLINE=95331781; PubMed=7612006;

RA Mazurk K., Schoen T.J., Chader G.J., Rodriguez I.R.;

RA "Structural organization and expression of the human

RT phosphatidylinositol-specific phospholipase C beta-3 gene.";

RL Biochem. Biophys. Res. Commun. 212:190-195(1995).

RN [2]

RX MEDLINE=95331781; PubMed=7607669;

RA Lagercrantz J., Carlson E., Phelan C., Grimmond S., Rosen A.,

RA Dare E., Nordenskjöld M., Hayward N.K., Larsson C., Weber G.;

RT "Genomic organization and complete cDNA sequence of the human

RT phosphoinositide-specific phospholipase C beta 3 gene (PLCB3).";

RL Genomics 26:467-472(1995).

RN [3]

RX MEDLINE=95331781; PubMed=7607669;

RA Carozzi A.J., Kriz R.W., Webster C., Parker P.J.;

RT "Identification, purification and characterization of a novel

RT phosphatidylinositol-specific phospholipase C, a third member of the

RT beta subfamily.";

RL Eur. J. Biochem. 210:521-529(1992).

RN [4]

RX MEDLINE=95331781; PubMed=7607669;

RA Carozzi A.J., Kriz R.W., Webster C., Parker P.J.;

RT "Identification, purification and characterization of a novel

RT phosphatidylinositol-specific phospholipase C, a third member of the

RT beta subfamily.";

RL Eur. J. Biochem. 210:521-529(1992).

RN [4]

RX MEDLINE=95331781; PubMed=7607669;

RA Carozzi A.J., Kriz R.W., Webster C., Parker P.J.;

RT "Identification, purification and characterization of a novel

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RN [4]

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RT beta subfamily.";

RL Eur. J. Biochem. 210:521-529(1992).

RN [4]

RX MEDLINE=95331781; PubMed=7607669;

RA Carozzi A.J., Kriz R.W., Webster C., Parker P.J.;

RT "Identification, purification and characterization of a novel</

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Matches 163; Conservative 94; Mismatches 231; Indels 138; Gaps 23;

23 EVFTYSR-----NRMASGELLKFLHTEQGDVDFILDDAKQIWERIRKDWKKSFGGLASIN 78
   | | | | | : : : | | | | | | | | | | | | | | | | | | | | | | | |
367 EIVDFEYTSRSGKMSLEQFRHFLTSQ-----KALRDSISRTIIVVSFCS 413
   | | | | | : : : | | | | | | | | | | | | | | | | | | | | | | | |
79 SLLSKEA--FRKYLMPDNLGVLHN-----VVHODMTPQMSHYFTFTGHNSYLTGNQLSS 131
   | | | | | : : : | | | | | | | | | | | | | | | | | | | | | | | |

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Db 414 NDDSKMGLIEFTSLLSP-----HNSPVVPVIODMSPRLNEYLSSSHNTYLLGQFGG 467
Qy 132 DSSDTPIAAALRRGVVVELDLPDDKGMKVTHGNTLTNPVSFKQCVTAIKNNAFTSE 191
Db 468 ESSIEGYIRSLQKCKIEIDCW-DGPNPVPVCHGHTFTSMIKENDVIDAIRKYAFVSP 526
Qy 192 YPVCVTIEDHLTSELQGHAAETLEILGDALYYPPTTDALVEEFPSPESLKRKIIISTKPP 251
Db 527 YPLFISLEIHCCPDQORQMVSMKQAFGDTLVKRPVTANESVLPSPEDLLNKILLKVK-- 584
Qy 252 KEYLEACSTQKLAMENRNIVELEKEDEKLEQTFAPLEENHILGENTPSLKEVEVLSQK 311
Db 585 -----CSATPLHOFSTDILKVGITDSDTTESSELENSLTG-----LRK-----GKR 628
Qy 312 EMST--PAELNSRSPDLGEATSTRYKSNNDGNDNPKHKYARLITIRLAKHAKGTSMEH 369
Db 629 RMKNIIVQELQQLAP-----YARSLKFR----- 651
Qy 370 RLQVDESVKRISLESKL-----EKVVEKWPEALV-----KFTQKNILRVYPAANRVN 417
Db 652 -----NFSLPESKTYSHIFSERTIKKHGKAMVPRLSKHNLRYLCRYPGPLRVG 702
Qy 418 SSNFCPTLAWNYQAQVMAQNGYKELWQAFGKFKGNGCGVYLPK--QYLL-----E 469
Db 703 STNFPQVYWRGLGYOMVALNWQYDTGLQINDALFTADPTGYLLKPPCORIIGTVGEE 762
Qy 470 NLPSGVFPNTPSPRNTTILKIKVMTTLGWDKAFSKRHFDLFSPPDFFTRVIVGVPADE 529
Db 763 GLPRKIK-----LTIDVISGQQLRRARELSNSETLSP---YVEIQVHSMEEESP 807
Qy 530 AKWTSVY-DNSWAPHWNED--HEFALKCPELALLRIEVRDHDHDDSKDE-FEGOTCLPIH 585
Db 808 FRWCSKVVHENGFRFPWGTWVYESIISDDFYSMIRFLVHHRGNSGNDISIFANFTC-PID 866
Qy 586 EVRDGYRCMQMYDKKG-NVLKGVLM 610
Db 867 RLQOQYRHIRLDMQGENLFLSLFL 892

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Search completed: July 26, 2002, 17:28:04
Job time: 382 sec